

	BRACE2007518//	0	//	0.000	//	2.707
	BRACE2007798//	0	//	0.000	//	1.234
	BRACE2008653//	0	//	0.000	//	4.403
	BRACE2008941//	0	//	0.000	//	11.920
5	BRACE2009037//	0	//	0.000	//	0.697
	BRACE2009517//	0	//	0.000	//	6.470
	BRACE2011183//	0	//	0.000	//	7.667
	BRACE2012528//	0	//	0.000	//	0.566
	BRACE2017397//	0	//	0.000	//	11.252
10	BRACE2017574//	0	//	0.000	//	6.110
	BRACE2019147//	0	//	0.000	//	2.554
	BRACE2020584//	0	//	0.000	//	62.692
	BRACE2022333//	0	//	0.000	//	10.589
	BRACE2022638//	0	//	0.000	//	2.667
15	BRACE2027896//	0	//	0.000	//	30.503
	BRACE2030341//	0	//	0.000	//	16.499
	BRACE2037310//	0	//	0.000	//	23.401
	BRACE2045445//	0	//	0.000	//	62.692
	BRACE3004371//	0	//	0.000	//	4.481
20	BRACE3005938//	0	//	0.000	//	1.313
	BRACE3007258//	0	//	0.000	//	15.521
	BRACE3008772//	0	//	0.000	//	62.692
	BRACE3010428//	0	//	0.000	//	5.461
	BRACE3027478//	0	//	0.000	//	19.089
25	BRACE3040863//	0	//	0.000	//	21.335
	BRALZ2009446//	0	//	0.000	//	5.561
	BRALZ2009482//	0	//	0.000	//	0.443
	BRALZ2017359//	0	//	0.000	//	24.816
	BRAMY2000585//	0	//	0.000	//	2.929
30	BRAMY2004363//	0	//	0.000	//	12.191
	BRAMY2004521//	0	//	0.000	//	5.654
	BRAMY2006366//	0	//	0.000	//	10.987
	BRAMY2009123//	0	//	0.000	//	54.206
	BRAMY2009934//	0	//	0.000	//	7.051
35	BRAMY2011105//	67.510	//	0	//	0.000
	BRAMY2012536//	0	//	0.000	//	0.688

	BAMY2013659//	0	//	0.000	//	34.645
	BAMY2019989//	0	//	0.000	//	1.150
	BAMY2020427//	0	//	0.000	//	0.706
	BAMY2022168//	0	//	0.000	//	16.134
5	BAMY2026685//	0	//	0.000	//	2.956
	BAMY2028740//	0	//	0.000	//	1.110
	BAMY2031516//	0	//	0.000	//	8.809
	BAMY2032087//	0	//	0.000	//	4.333
	BAMY2040095//	0	//	0.000	//	0.815
10	BAMY3002458//	0	//	0.000	//	14.807
	BAMY3005184//	0	//	0.000	//	26.725
	BRAWH1000040//	0	//	0.000	//	2.462
	BRAWH1000093//	10.279	//	0	//	2.200
	BRAWH2000082//	0	//	0.000	//	0.457
15	BRAWH2000488//	0	//	0.000	//	12.025
	BRAWH2000588//	0	//	0.000	//	1.496
	BRAWH2000633//	0	//	0.000	//	1.581
	BRAWH2000697//	0	//	0.000	//	1.206
	BRAWH2000839//	0	//	0.000	//	0.980
20	BRAWH2001092//	0	//	0.000	//	1.677
	BRAWH2001141//	0	//	0.000	//	6.061
	BRAWH2001412//	0	//	0.000	//	17.933
	BRAWH2001439//	0	//	0.000	//	1.227
	BRAWH2002601//	0	//	0.000	//	5.932
25	BRAWH2003693//	0	//	0.000	//	4.080
	BRAWH2004078//	0	//	0.000	//	6.285
	BRAWH2005578//	0	//	0.000	//	15.983
	BRAWH2005661//	0	//	0.000	//	1.907
	BRAWH2007605//	0	//	0.000	//	2.446
30	BRAWH2008058//	0	//	0.000	//	27.939
	BRAWH2009238//	0	//	0.000	//	6.217
	BRAWH2011343//	0	//	0.000	//	8.367
	BRAWH2012698//	0	//	0.000	//	22.868
	BRAWH2014188//	0	//	0.000	//	11.100
35	BRAWH2014473//	0	//	0.000	//	54.394
	BRAWH2014645//	0	//	0.000	//	2.522

	BRAWH2016166//	0	//	0.000	//	18.040
	BRAWH2017304//	0	//	0.000	//	19.804
	BRAWH2017685//	0	//	0.000	//	1.211
	BRAWH2018526//	0	//	0.000	//	0.367
5	BRAWH2018745//	0	//	0.000	//	54.394
	BRAWH3000314//	0	//	0.000	//	28.447
	BRAWH3001326//	0	//	0.000	//	54.394
	BRAWH3002574//	0	//	0.000	//	7.885
	BRAWH3002853//	0	//	0.000	//	1.764
10	BRAWH3003727//	0	//	0.000	//	11.993
	BRAWH3004350//	0	//	0.000	//	19.774
	BRAWH3016271//	0	//	0.000	//	6.433
	BRAWH3021545//	0	//	0.000	//	17.404
	BRAWH3026529//	0	//	0.000	//	54.394
15	BRAWH3029806//	0	//	0.000	//	10.629
	BRCAN2003944//	0	//	0.000	//	0.336
	BRCAN2009432//	29.345	//	0	//	3.141
	BRCAN2011946//	0	//	0.000	//	7.542
	BRCAN2021024//	0	//	0.000	//	24.461
20	BRCAN2022126//	0	//	0.000	//	5.791
	BRCAN2024572//	0	//	0.000	//	3.257
	BRCAN2028355//	0	//	0.000	//	1.762
	BRCOC1000040//	0	//	0.000	//	14.069
	BRCOC2000333//	0	//	0.000	//	14.286
25	BRCOC2003187//	0	//	0.000	//	0.938
	BRCOC2010730//	0	//	0.000	//	12.892
	BRCOC2012172//	0	//	0.000	//	6.710
	BRCOC2012551//	0	//	0.000	//	8.602
	BRCOC2015597//	0	//	0.000	//	25.187
30	BRHIP2001099//	0	//	0.000	//	8.268
	BRHIP2003062//	0	//	0.000	//	56.647
	BRHIP2007305//	0	//	0.000	//	1.350
	BRHIP2010487//	91.660	//	0	//	0.000
	BRHIP2010571//	0	//	0.000	//	18.366
35	BRHIP2011491//	0	//	0.000	//	0.986
	BRHIP2011616//	0	//	0.000	//	53.896

	BRHIP2015245//	0	//	0.000	//	5.663
	BRHIP2018712//	0	//	0.000	//	9.661
	BRHIP2019149//	0	//	0.000	//	13.172
	BRHIP2020799//	0	//	0.000	//	12.072
5	BRHIP2021762//	0	//	0.000	//	6.646
	BRHIP2022228//	0	//	0.000	//	10.898
	BRHIP2022326//	0	//	0.000	//	1.015
	BRHIP2023888//	0	//	0.000	//	0.439
	BRHIP2024742//	0	//	0.000	//	1.487
10	BRHIP2024911//	0	//	0.000	//	11.054
	BRHIP2027017//	0	//	0.000	//	13.730
	BRHIP3000017//	0	//	0.000	//	15.777
	BRHIP3000377//	0	//	0.000	//	6.870
	BRHIP3001076//	0	//	0.000	//	53.896
15	BRHIP3002141//	0	//	0.000	//	18.713
	BRHIP3005307//	0	//	0.000	//	53.896
	BRHIP3007223//	0	//	0.000	//	2.405
	BRHIP3007586//	0	//	0.000	//	4.116
	BRHIP3008344//	0	//	0.000	//	53.896
20	BRHIP3008565//	0	//	0.000	//	53.896
	BRHIP3012997//	0	//	87.379	//	0.000
	BRHIP3017855//	0	//	0.000	//	27.401
	BRHIP3020046//	0	//	0.000	//	1.208
	BRSSN2000295//	0	//	0.000	//	8.260
25	BRSSN2000498//	0	//	0.000	//	2.610
	BRSSN2001213//	0	//	0.000	//	24.268
	BRSSN2001869//	0	//	0.000	//	3.600
	BRSSN2006892//	0	//	0.000	//	18.468
	BRSSN2009518//	0	//	0.000	//	2.054
30	BRSSN2010019//	0	//	0.000	//	13.842
	BRSSN2014685//	0	//	0.000	//	16.936
	BRSSN2017422//	0	//	0.000	//	17.148
	BRSTN2001067//	0	//	0.000	//	7.384
	BRSTN2010089//	0	//	0.000	//	7.869
35	BRSTN2011961//	0	//	0.000	//	0.345
	BRSTN2012069//	3.583	//	1.784	//	0.271



	BRSTN2012174//	0	//	0.000	//	0.482
	BRSTN2013502//	0	//	0.000	//	5.797
	BRSTN2013931//	0	//	0.000	//	3.457
	BRSTN2016470//	0	//	0.000	//	0.522
5	BRSTN2016892//	0	//	0.000	//	3.559
	BRTHA2000057//	0	//	0.000	//	51.819
	BRTHA2004361//	0	//	0.000	//	51.819
	BRTHA2005831//	0	//	0.000	//	51.819
	BRTHA2005864//	0	//	0.000	//	1.935
10	BRTHA2010608//	0	//	0.000	//	51.819
	BRTHA2012183//	0	//	0.000	//	51.819
	BRTHA2012714//	0	//	0.000	//	5.980
	BRTHA2017178//	0	//	0.000	//	51.819
	BRTHA3003023//	0	//	0.000	//	2.410
15	BRTHA3003074//	0	//	0.000	//	13.429
	BRTHA3003736//	0	//	0.000	//	5.131
	BRTHA3004307//	0	//	0.000	//	17.964
	BRTHA3011265//	0	//	0.000	//	10.176
	BRTHA3020314//	0	//	0.000	//	12.144
20	BRTHA3023403//	0	//	0.000	//	26.579
	BRTHA3026507//	0	//	0.000	//	4.167
	BRTHA3027879//	0	//	0.000	//	51.819
	CHONS2002829//	0	//	0.000	//	11.691
	CTONG1000052//	0	//	0.000	//	2.162
25	CTONG1000087//	0	//	0.000	//	2.494
	CTONG1000094//	0	//	0.000	//	0.464
	CTONG1000137//	0	//	0.000	//	39.037
	CTONG1000180//	0	//	0.000	//	28.641
	CTONG1000241//	0	//	0.000	//	7.590
30	CTONG1000277//	0	//	0.000	//	24.668
	CTONG1000467//	0	//	0.000	//	10.248
	CTONG2000411//	0	//	0.000	//	6.864
	CTONG2000508//	0	//	0.000	//	4.709
	CTONG2001748//	0	//	0.000	//	2.493
35	CTONG2001932//	0	//	0.000	//	12.322
	CTONG2002073//	32.643	//	0	//	1.747

	CTONG2002270//	0	//	0.000	//	0.633
	CTONG2002744//	0	//	0.000	//	0.702
	CTONG2002766//	0	//	0.000	//	14.092
	CTONG2002803//	32.814	//	0	//	0.000
5	CTONG2003298//	0	//	0.000	//	1.731
	CTONG2003348//	0	//	0.000	//	39.037
	CTONG2003517//	0	//	0.000	//	13.371
	CTONG2003524//	0	//	0.000	//	1.922
	CTONG2004423//	0	//	0.000	//	13.705
10	CTONG2005145//	0	//	0.000	//	29.265
	CTONG2005615//	0	//	0.000	//	5.671
	CTONG2006235//	0	//	0.000	//	1.954
	CTONG2006377//	0	//	0.000	//	14.002
	CTONG2006562//	0	//	0.000	//	5.010
15	CTONG2006932//	0	//	0.000	//	2.625
	CTONG2007078//	0	//	0.000	//	3.048
	CTONG2007500//	0	//	0.000	//	8.072
	CTONG2008343//	0	//	0.000	//	39.037
	CTONG2008398//	0	//	0.000	//	0.912
20	CTONG2008518//	0	//	0.000	//	4.593
	CTONG2008689//	0	//	0.000	//	24.924
	CTONG2009529//	0	//	0.000	//	7.541
	CTONG2009923//	0	//	0.000	//	39.037
	CTONG2009938//	0	//	0.000	//	23.863
25	CTONG2010348//	0	//	0.000	//	6.336
	CTONG2010408//	0	//	0.000	//	10.219
	CTONG2010649//	0	//	0.000	//	5.595
	CTONG2010821//	0	//	0.000	//	2.557
	CTONG2011801//	0	//	0.000	//	3.532
30	CTONG2011825//	0	//	0.000	//	10.239
	CTONG2012452//	7.936	//	0	//	0.000
	CTONG2012847//	38.378	//	0	//	2.054
	CTONG2012879//	0	//	0.000	//	4.056
	CTONG2012996//	0	//	0.000	//	3.482
35	CTONG2013128//	0	//	0.000	//	39.037
	CTONG2013156//	0	//	0.000	//	24.668

	CTONG2013907//	0	//	0.000	//	2.571
	CTONG2013934//	0	//	0.000	//	8.273
	CTONG2014369//	0	//	0.000	//	4.963
	CTONG2014898//	0	//	0.000	//	13.759
5	CTONG2015345//	0	//	0.000	//	10.182
	CTONG2016056//	0	//	0.000	//	2.372
	CTONG2016408//	0	//	0.000	//	4.416
	CTONG2016575//	0	//	0.000	//	1.779
	CTONG2016869//	0	//	0.000	//	3.150
10	CTONG2017094//	0	//	0.000	//	2.666
	CTONG2017429//	0	//	0.000	//	8.607
	CTONG2017998//	0	//	0.000	//	5.976
	CTONG2018211//	0	//	0.000	//	4.068
	CTONG2018637//	0	//	0.000	//	15.649
15	CTONG2018898//	0	//	0.000	//	2.298
	CTONG2019822//	0	//	0.000	//	7.755
	CTONG2020378//	0	//	0.000	//	19.250
	CTONG2020411//	0	//	0.000	//	32.844
	CTONG2020484//	0	//	55.423	//	0.000
20	CTONG2020560//	0	//	0.000	//	5.368
	CTONG2024031//	0	//	0.000	//	6.165
	CTONG2027263//	0	//	0.000	//	19.641
	CTONG2028124//	0	//	0.000	//	2.997
	CTONG3001123//	0	//	0.000	//	9.359
25	CTONG3002518//	0	//	0.000	//	10.064
	CTONG3004317//	0	//	0.000	//	39.037
	CTONG3008894//	0	//	0.000	//	0.867
	CTONG3009028//	0	//	0.000	//	3.839
	CTONG3009239//	0	//	0.000	//	1.722
30	D30ST3000258//	0	//	0.000	//	22.242
	D60ST2000464//	0	//	0.000	//	1.307
	D90ST2002608//	0	//	0.000	//	2.657
	D90ST2003791//	0	//	0.000	//	7.297
	DFNES1000185//	29.393	//	0	//	0.000
35	DFNES2000011//	0	//	0.000	//	4.565
	DFNES2000426//	0	//	0.000	//	15.059

	DFNES2000443//	0	//	0.000	//	0.810
	DFNES2001829//	0	//	0.000	//	11.006
	DFNES2006346//	0	//	0.000	//	8.425
	DFNES2007634//	0	//	0.000	//	7.421
5	FCBBF1000024//	0	//	0.000	//	5.237
	FCBBF1000027//	0	//	0.000	//	2.621
	FCBBF1000061//	0	//	0.000	//	2.805
	FCBBF1000182//	0	//	0.000	//	10.114
	FCBBF1000197//	0	//	0.000	//	2.548
10	FCBBF1000294//	0	//	0.000	//	1.284
	FCBBF1000367//	0	//	0.000	//	1.812
	FCBBF1000412//	0	//	0.000	//	2.308
	FCBBF1000425//	0	//	0.000	//	6.226
	FCBBF1000466//	14.193	//	0	//	0.760
15	FCBBF1000574//	0	//	0.000	//	4.952
	FCBBF1000760//	0	//	0.000	//	0.781
	FCBBF2000087//	0	//	0.000	//	3.441
	FCBBF2000591//	0	//	0.000	//	0.342
	FCBBF2000685//	0	//	0.000	//	8.114
20	FCBBF2000885//	0	//	0.000	//	3.661
	FCBBF2001001//	0	//	0.000	//	11.399
	FCBBF2001291//	0	//	0.000	//	2.269
	FCBBF2006380//	0	//	0.000	//	39.231
	FCBBF3000115//	0	//	0.000	//	9.520
25	FCBBF3000536//	0	//	0.000	//	3.179
	FCBBF3001470//	0	//	0.000	//	1.619
	FCBBF3003800//	0	//	0.000	//	1.409
	FCBBF3004473//	25.604	//	0	//	1.370
	FCBBF3004847//	0	//	0.000	//	39.231
30	FCBBF3006821//	0	//	0.000	//	13.636
	FCBBF3007244//	0	//	0.000	//	9.258
	FCBBF3007859//	0	//	0.000	//	7.748
	FCBBF3008153//	0	//	0.000	//	6.525
	FCBBF3010695//	0	//	0.000	//	2.958
35	FCBBF3016928//	0	//	0.000	//	1.045
	FCBBF3017396//	0	//	0.000	//	7.305

	FCBBF3017531// 0 // 0.000 // 1.912
	FCBBF3018796// 0 // 0.000 // 7.405
	FCBBF3019714// 0 // 0.000 // 2.443
	FCBBF3019839// 0 // 0.000 // 17.866
5	FCBBF3021807// 0 // 0.000 // 5.171
	FCBBF3023667// 0 // 0.000 // 0.317
	FCBBF3024002// 0 // 0.000 // 6.769
	FCBBF3024623// 0 // 0.000 // 6.682
	FCBBF3025528// 0 // 0.000 // 5.758
10	FCBBF3025568// 0 // 0.000 // 19.615
	FCBBF3025737// 0 // 0.000 // 7.752
	FCBBF3025905// 0 // 0.000 // 19.079
	FCBBF4000142// 0 // 0.000 // 4.360
	FCBBF4000446// 0 // 0.000 // 0.896
15	FCBBF5000261// 0 // 0.000 // 6.193
	FEBRA1000022// 0 // 0.000 // 12.554
	FEBRA1000088// 0 // 0.000 // 5.090
	FEBRA2000105// 0 // 0.000 // 1.711
	FEBRA2000129// 0 // 0.000 // 3.100
20	FEBRA2000210// 0 // 0.000 // 0.843
	FEBRA2000462// 0 // 0.000 // 6.733
	FEBRA2000510// 0 // 0.000 // 4.401
	FEBRA2000536// 0 // 0.000 // 3.757
	FEBRA2000581// 0 // 0.000 // 0.949
25	FEBRA2000680// 0 // 0.000 // 33.628
	FEBRA2000733// 3.756 // 0 // 1.206
	FEBRA2000740// 0 // 0.000 // 9.442
	FEBRA2000757// 0 // 0.000 // 3.652
	FEBRA2000856// 0 // 0.000 // 18.931
30	FEBRA2000880// 0 // 0.000 // 12.639
	FEBRA2001745// 0 // 0.000 // 1.495
	FEBRA2001828// 0 // 0.000 // 6.489
	FEBRA2002527// 0 // 0.000 // 3.416
	FEBRA2003436// 0 // 0.000 // 6.630
35	FEBRA2003750// 0 // 0.000 // 19.596
	FEBRA2003833// 0 // 0.000 // 14.436

	FEBRA2003926//	0	//	0.000	//	4.163
	FEBRA2004042//	47.274	//	0	//	0.000
	FEBRA2004412//	0	//	0.000	//	3.502
	FEBRA2004852//	0	//	0.000	//	32.361
5	FEBRA2005752//	0	//	0.000	//	4.964
	FEBRA2006092//	0	//	0.000	//	2.225
	FEBRA2007714//	0	//	0.000	//	9.952
	FEBRA2007818//	0	//	0.000	//	6.669
	FEBRA2007901//	0	//	0.000	//	4.420
10	FEBRA2008081//	0	//	0.000	//	0.845
	FEBRA2008087//	3.995	//	0	//	0.214
	FEBRA2008210//	0	//	0.000	//	15.999
	FEBRA2008255//	0	//	0.000	//	6.035
	FEBRA2008302//	0	//	0.000	//	1.269
15	FEBRA2008583//	0	//	0.000	//	0.315
	FEBRA2009419//	0	//	0.000	//	1.576
	FEBRA2011090//	0	//	0.000	//	20.700
	FEBRA2011392//	0	//	0.000	//	32.361
	FEBRA2014417//	0	//	0.000	//	1.288
20	FEBRA2022055//	0	//	0.000	//	5.712
	FEBRA2022504//	0	//	0.000	//	1.959
	FEBRA2023927//	0	//	0.000	//	4.858
	FEBRA2025838//	0	//	0.000	//	0.980
	FEBRA2026984//	0	//	0.000	//	20.914
25	FEBRA2028516//	0	//	0.000	//	1.364
	FELIV1000153//	0	//	0.000	//	0.197
	HCASM2000016//	0	//	0.000	//	1.780
	HCASM2000138//	0	//	0.000	//	10.075
	HCASM2000363//	0	//	0.000	//	0.811
30	HCASM2001890//	0	//	0.000	//	15.228
	HCASM2008536//	0	//	0.000	//	15.228
	HCHON1000030//	0	//	0.000	//	0.216
	HCHON1000131//	0	//	0.000	//	9.787
	HCHON1000142//	0	//	0.000	//	15.860
35	HCHON2000056//	0	//	0.000	//	1.353
	HCHON2000087//	0	//	58.329	//	0.738

	HCHON2000160//	0	//	0.000	//	1.201
	HCHON2000226//	0	//	0.000	//	0.962
	HCHON2000244//	0	//	0.000	//	1.569
	HCHON2000265//	0	//	0.000	//	2.413
5	HCHON2000295//	0	//	0.000	//	1.045
	HCHON2000323//	0	//	0.000	//	2.209
	HCHON2000418//	0	//	0.000	//	15.860
	HCHON2000475//	0	//	0.000	//	3.175
	HCHON2000626//	0	//	0.000	//	5.608
10	HCHON2000698//	0	//	0.000	//	10.256
	HCHON2000738//	0	//	0.000	//	3.551
	HCHON2000743//	0	//	0.000	//	7.282
	HCHON2000826//	0	//	0.000	//	0.854
	HCHON2001039//	0	//	0.000	//	2.662
15	HCHON2001084//	0	//	0.000	//	2.739
	HCHON2001200//	0	//	40.779	//	1.032
	HCHON2001217//	0	//	0.000	//	4.966
	HCHON2001434//	0	//	0.000	//	3.644
	HCHON2001505//	0	//	0.000	//	16.079
20	HCHON2001598//	0	//	0.000	//	5.796
	HCHON2001665//	0	//	0.000	//	1.840
	HCHON2001853//	0	//	0.000	//	6.680
	HCHON2002247//	0	//	0.000	//	3.348
	HCHON2004002//	0	//	0.000	//	0.936
25	HCHON2005921//	0	//	0.000	//	24.732
	HCHON2006250//	34.872	//	0	//	0.000
	HCHON2007650//	0	//	0.000	//	7.263
	HCHON2008444//	0	//	0.000	//	15.860
	HEART1000149//	0	//	0.000	//	4.480
30	HEART1000185//	0	//	0.000	//	5.657
	HEART2000506//	0	//	0.000	//	4.183
	HEART2004931//	0	//	0.000	//	8.110
	HEART2007231//	0	//	0.000	//	11.555
	HHDPC1000114//	0	//	0.000	//	0.867
35	HHDPC1000163//	0	//	0.000	//	1.500
	HHDPC2000455//	0	//	0.000	//	3.932

	HHDPC2000572//	0	//	0.000	//	7.809
	HHDPC2000656//	0	//	0.000	//	10.195
	HHDPC2003439//	0	//	0.000	//	1.517
	HHDPC2003983//	0	//	0.000	//	2.657
5	HHDPC2007267//	0	//	0.000	//	0.582
	HHDPC2007775//	0	//	0.000	//	12.888
	HLUNG1000055//	0	//	0.000	//	1.937
	HLUNG1000064//	0	//	0.000	//	8.121
	HLUNG1000076//	0	//	0.000	//	1.003
10	HLUNG2000004//	0	//	0.000	//	3.017
	HLUNG2000063//	0	//	0.000	//	5.883
	HLUNG2000314//	0	//	0.000	//	5.852
	HLUNG2000412//	0	//	0.000	//	3.194
	HLUNG2000501//	0	//	0.000	//	1.023
15	HLUNG2000846//	0	//	0.000	//	5.388
	HLUNG2000884//	0	//	0.000	//	2.553
	HLUNG2001146//	0	//	0.000	//	6.252
	HLUNG2001507//	0	//	0.000	//	5.972
	HLUNG2001518//	0	//	0.000	//	5.217
20	HLUNG2001677//	0	//	0.000	//	4.191
	HLUNG2002648//	0	//	0.000	//	4.311
	HLUNG2002811//	0	//	0.000	//	2.906
	HLUNG2003003//	0	//	0.000	//	28.594
	HLUNG2004159//	0	//	0.000	//	2.162
25	HLUNG2004170//	0	//	0.000	//	7.349
	HLUNG2004684//	75.236	//	0	//	0.000
	HLUNG2006812//	0	//	0.000	//	7.053
	HLUNG2008333//	0	//	0.000	//	24.539
	HLUNG2008637//	0	//	0.000	//	2.015
30	HLUNG2009225//	0	//	0.000	//	5.396
	HLUNG2015184//	0	//	0.000	//	15.617
	HLUNG2017262//	0	//	0.000	//	3.783
	HSYRA1000062//	0	//	0.000	//	0.511
	HSYRA1000152//	0	//	0.000	//	1.423
35	HSYRA1000178//	0	//	0.000	//	2.991
	HSYRA2000159//	0	//	0.000	//	0.719



	HSYRA2000224//	0	//	0.000	//	2.145
	HSYRA2000232//	0	//	0.000	//	0.882
	HSYRA2000248//	0	//	0.000	//	4.053
	HSYRA2000255//	0	//	0.000	//	2.141
5	HSYRA2000640//	0	//	0.000	//	4.064
	HSYRA2000743//	0	//	0.000	//	10.153
	HSYRA2001105//	0	//	0.000	//	3.286
	HSYRA2001138//	0	//	0.000	//	0.304
	HSYRA2001396//	0	//	0.000	//	5.436
10	HSYRA2001476//	0	//	0.000	//	5.182
	HSYRA2001567//	0	//	0.000	//	2.673
	HSYRA2001574//	0	//	0.000	//	0.897
	HSYRA2001580//	0	//	0.000	//	13.073
	HSYRA2001615//	0	//	0.000	//	2.473
15	HSYRA2001621//	0	//	17.301	//	0.000
	HSYRA2007650//	0	//	0.000	//	5.673
	IMR321000158//	0	//	0.000	//	1.816
	IMR321000210//	0	//	0.000	//	1.209
	IMR321000219//	0	//	0.000	//	3.013
20	IMR321000242//	0	//	0.000	//	6.707
	IMR321000266//	0	//	0.000	//	3.375
	IMR322000121//	0	//	0.000	//	1.330
	IMR322000730//	3.055	//	0	//	0.327
	IMR322000935//	0	//	0.000	//	1.786
25	IMR322001049//	0	//	0.000	//	6.909
	IMR322001435//	0	//	0.000	//	3.361
	IMR322001534//	0	//	0.000	//	9.855
	IMR322001600//	0	//	15.181	//	0.960
	IMR322001710//	0	//	0.000	//	2.313
30	IMR322001879//	0	//	0.000	//	11.495
	IMR322019070//	0	//	0.000	//	3.191
	KIDNE1000036//	0	//	0.000	//	25.490
	KIDNE1000145//	0	//	0.000	//	16.491
	KIDNE2000085//	0	//	0.000	//	3.679
35	KIDNE2000330//	76.084	//	0	//	0.000
	KIDNE2000403//	0	//	0.000	//	1.971

	KIDNE2001162// 0 // 0.000 // 1.670
	KIDNE2001467// 0 // 0.000 // 0.933
	KIDNE2001979// 0 // 0.000 // 7.027
	KIDNE2002252// 0 // 0.000 // 2.600
5	KIDNE2003305// 0 // 0.000 // 1.004
	KIDNE2003941// 0 // 0.000 // 0.602
	KIDNE2005321// 0 // 0.000 // 11.785
	KIDNE2005676// 0 // 0.000 // 5.034
	KIDNE2006014// 0 // 0.000 // 3.541
10	KIDNE2006030// 0 // 0.000 // 7.636
	KIDNE2006248// 0 // 0.000 // 1.112
	KIDNE2006465// 0 // 0.000 // 3.690
	KIDNE2007040// 0 // 0.000 // 25.490
	KIDNE2007328// 0 // 0.000 // 2.110
15	KIDNE2007352// 0 // 0.000 // 0.992
	KIDNE2007811// 0 // 0.000 // 10.218
	KIDNE2007954// 0 // 0.000 // 2.514
	KIDNE2008048// 0 // 0.000 // 3.839
	KIDNE2009367// 0 // 0.000 // 9.888
20	KIDNE2009605// 0 // 0.000 // 18.012
	KIDNE2010049// 76.623 // 0 // 4.101
	KIDNE2012784// 0 // 0.000 // 40.625
	KIDNE2013158// 0 // 0.000 // 21.635
	KIDNE2013845// 0 // 0.000 // 2.666
25	KIDNE2014290// 0 // 0.000 // 3.345
	KIDNE2014325// 0 // 0.000 // 4.512
	KIDNE2017040// 0 // 0.000 // 4.011
	LIVER1000079// 0 // 0.000 // 2.090
	LIVER1000132// 0 // 0.000 // 0.597
30	LIVER2000033// 0 // 0.000 // 1.650
	LIVER2001539// 0 // 0.000 // 5.939
	LIVER2001608// 29.267 // 0 // 1.566
	LIVER2002842// 0 // 0.000 // 9.107
	LIVER2003234// 0 // 0.000 // 12.095
35	LIVER2005218// 0 // 0.000 // 5.883
	LIVER2007783// 0 // 0.000 // 4.894

	LIVER2008465//	0	//	0.000	//	7.893
	MAMGL1000083//	0	//	0.000	//	0.346
	MESAN2000264//	0	//	0.000	//	2.350
	MESAN2000267//	0	//	0.000	//	2.930
5	MESAN2000894//	0	//	0.000	//	24.337
	MESAN2001154//	0	//	0.000	//	1.589
	MESAN2002086//	0	//	0.000	//	2.482
	MESAN2002424//	0	//	0.000	//	24.337
	MESAN2002724//	0	//	0.000	//	5.499
10	MESAN2002844//	0	//	0.000	//	8.642
	MESAN2003039//	0	//	0.000	//	19.415
	MESAN2003058//	0	//	0.000	//	7.143
	MESAN2003444//	0	//	0.000	//	8.886
	MESAN2003709//	0	//	0.000	//	9.892
15	MESAN2005303//	0	//	0.000	//	9.449
	MESAN2005957//	0	//	0.000	//	17.666
	MESAN2006043//	0	//	0.000	//	9.499
	MESAN2006580//	0	//	0.000	//	24.337
	MESAN2006743//	0	//	0.000	//	13.792
20	MESAN2009580//	0	//	0.000	//	1.325
	MESAN2013284//	0	//	0.000	//	2.930
	MESAN2014295//	0	//	0.000	//	24.337
	MESAN2016552//	0	//	0.000	//	14.511
	MESAN2017152//	0	//	0.000	//	24.337
25	NB9N41000121//	16.735	//	0	//	0.000
	NB9N42000281//	0	//	0.000	//	2.280
	NOVAR1000015//	0	//	0.000	//	3.622
	NOVAR1000091//	0	//	0.000	//	2.310
	NOVAR2000710//	0	//	0.000	//	4.201
30	NT2NE1000163//	0	//	0.000	//	2.899
	NT2NE2000056//	8.755	//	0	//	3.280
	NT2NE2000327//	0	//	0.000	//	3.000
	NT2NE2000383//	0	//	0.000	//	5.437
	NT2NE2000384//	0	//	0.000	//	2.745
35	NT2NE2000455//	0	//	0.000	//	24.761
	NT2NE2000575//	0	//	0.000	//	1.720

	NT2NE2000707//	0	//	0.000	//	1.596
	NT2NE2000963//	5.112	//	0	//	0.547
	NT2NE2001000//	0	//	0.000	//	2.053
	NT2NE2001176//	0	//	0.000	//	1.362
5	NT2NE2001337//	0	//	0.000	//	5.420
	NT2NE2001435//	0	//	0.000	//	5.072
	NT2NE2001545//	0	//	0.000	//	2.137
	NT2NE2001617//	0	//	0.000	//	5.411
	NT2NE2001660//	0	//	0.000	//	9.341
10	NT2NE2001793//	0	//	0.000	//	7.422
	NT2NE2002620//	0	//	90.183	//	0.000
	NT2NE2003185//	0	//	0.000	//	4.521
	NT2NE2003485//	0	//	0.000	//	-5.552
	NT2NE2003569//	0	//	0.000	//	2.070
15	NT2NE2004519//	0	//	0.000	//	2.137
	NT2NE2004716//	0	//	0.000	//	4.578
	NT2NE2005358//	0	//	0.000	//	24.761
	NT2NE2006458//	0	//	0.000	//	3.372
	NT2NE2006659//	0	//	0.000	//	21.581
20	NT2NE2009295//	0	//	0.000	//	2.379
	NT2NE2015974//	0	//	0.000	//	9.111
	NT2NE2017492//	0	//	0.000	//	20.127
	NT2RI1000127//	0	//	0.000	//	2.165
	NT2RI2000007//	0	//	0.000	//	39.625
25	NT2RI2000064//	0	//	0.000	//	3.210
	NT2RI2000282//	0	//	0.000	//	0.378
	NT2RI2000294//	0	//	0.000	//	2.257
	NT2RI2000344//	0	//	76.334	//	0.000
	NT2RI2000578//	7.452	//	31.528	//	0.399
30	NT2RI2000671//	0	//	0.000	//	1.255
	NT2RI2000685//	0	//	0.000	//	3.545
	NT2RI2000689//	34.460	//	0	//	1.844
	NT2RI2000727//	0	//	0.000	//	0.617
	NT2RI2001091//	0	//	0.000	//	4.193
35	NT2RI2001230//	0	//	0.000	//	0.920
	NT2RI2001540//	1.269	//	0	//	1.494

NT2RI2001657// 0 // 0.000 // 1.914  
NT2RI2001859// 0 // 0.000 // 1.157  
NT2RI2002091// 0.897 // 2.529 // 0.976  
NT2RI2002152// 0 // 0.000 // 3.000  
5 NT2RI2002316// 0 // 0.000 // 0.956  
NT2RI2002391// 18.073 // 0 // 0.000  
NT2RI2002654// 13.092 // 0 // 0.000  
NT2RI2002865// 0 // 0.000 // 8.087  
NT2RI2003304// 5.848 // 0 // 0.000  
10 NT2RI2003317// 0 // 0.000 // 3.760  
NT2RI2003338// 0 // 0.000 // 4.831  
NT2RI2003344// 0 // 0.000 // 6.968  
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15 NT2RI2003556// 0 // 0.000 // 0.908  
NT2RI2003695// 0 // 0.000 // 0.939  
NT2RI2003738// 0 // 0.000 // 1.252  
NT2RI2003751// 0 // 0.000 // 1.652  
NT2RI2004157// 0 // 0.000 // 39.625  
20 NT2RI2004188// 0 // 0.000 // 3.425  
NT2RI2004230// 0 // 0.000 // 6.843  
NT2RI2004535// 0 // 0.000 // 2.283  
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NT2RI2005335// 0 // 0.000 // 3.232  
25 NT2RI2005358// 0 // 0.000 // 24.478  
NT2RI2005405// 0 // 0.000 // 1.004  
NT2RI2005713// 0 // 0.000 // 1.764  
NT2RI2005723// 11.184 // 0 // 1.197  
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30 NT2RI2005814// 0 // 0.000 // 1.553  
NT2RI2005818// 0 // 0.000 // 3.038  
NT2RI2006412// 0 // 0.000 // 0.978  
NT2RI2006825// 0 // 0.000 // 3.270  
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35 NT2RI2007148// 0 // 0.000 // 2.253  
NT2RI2007277// 0 // 0.000 // 1.169

	NT2R12007384//	9.651	//	0	//	1.033
	NT2R12007445//	0	//	0.000	//	2.139
	NT2R12007498//	0	//	0.000	//	0.486
	NT2R12007589//	23.800	//	0	//	0.000
5	NT2R12007629//	0	//	0.000	//	2.404
	NT2R12007987//	0	//	0.000	//	2.147
	NT2R12008007//	0	//	0.000	//	23.084
	NT2R12008045//	0	//	0.000	//	0.926
	NT2R12008336//	0	//	0.000	//	0.956
10	NT2R12008481//	0	//	0.000	//	2.646
	NT2R12008526//	17.086	//	0	//	0.000
	NT2R12008724//	0	//	0.000	//	2.190
	NT2R12008749//	0	//	0.000	//	2.023
	NT2R12008791//	0	//	0.000	//	1.392
15	NT2R12008942//	0	//	0.000	//	16.259
	NT2R12009037//	0	//	0.000	//	1.005
	NT2R12009065//	10.408	//	0	//	0.000
	NT2R12009269//	0	//	0.000	//	1.179
	NT2R12009402//	0	//	0.000	//	7.482
20	NT2R12009406//	0	//	0.000	//	3.356
	NT2R12009583//	0	//	0.000	//	0.267
	NT2R12014247//	0	//	0.000	//	18.191
	NT2R12014733//	0	//	0.000	//	29.743
	NT2R12017529//	0	//	0.000	//	1.157
25	NT2R12022468//	0	//	0.000	//	7.995
	NT2R12024313//	0	//	0.000	//	17.475
	NT2R12027323//	0	//	0.000	//	39.625
	NT2R13001445//	0	//	0.000	//	7.554
	NT2R13005724//	0	//	0.000	//	7.069
30	NT2R13005923//	0	//	0.000	//	23.249
	NT2R13006284//	46.111	//	0	//	0.000
	NT2R13006340//	0	//	0.000	//	19.479
	NT2R13006666//	0	//	0.000	//	24.901
	NT2R13006673//	0	//	0.000	//	11.902
35	NT2R13007291//	0	//	0.000	//	14.928
	NT2R13007543//	0	//	0.000	//	1.012

	NT2RP6000017//	0	//	0.000	//	3.569
	NT2RP6000039//	0	//	0.000	//	4.277
	NT2RP6000059//	0	//	0.000	//	25.869
	NT2RP6000077//	0	//	0.000	//	30.666
5	NT2RP6000078//	0	//	0.000	//	0.429
	NT2RP6000085//	0	//	0.000	//	11.032
	NT2RP6000123//	0	//	0.000	//	0.467
	NT2RP7000069//	0	//	0.000	//	8.035
	NT2RP7000076//	0	//	0.000	//	0.727
10	NT2RP7000173//	0	//	0.000	//	0.663
	NT2RP7000477//	0	//	0.000	//	2.360
	NT2RP7000586//	0	//	0.000	//	13.104
	NT2RP7000600//	0	//	0.000	//	7.929
	NT2RP7000906//	0	//	0.000	//	3.112
15	NT2RP7001166//	0	//	0.000	//	2.676
	NT2RP7001962//	0	//	0.000	//	3.168
	NT2RP7002028//	0	//	0.000	//	7.190
	NT2RP7002376//	0	//	0.000	//	14.471
	NT2RP7002379//	0	//	0.000	//	2.402
20	NT2RP7002449//	0	//	0.000	//	2.409
	NT2RP7002802//	0	//	0.000	//	8.717
	NT2RP7002875//	0	//	0.000	//	1.101
	NT2RP7002982//	0	//	0.000	//	9.273
	NT2RP7003055//	0	//	0.000	//	12.585
25	NT2RP7003203//	0	//	0.000	//	4.406
	NT2RP7003319//	0	//	0.000	//	31.557
	NT2RP7003632//	0	//	0.000	//	1.942
	NT2RP7003647//	0	//	0.000	//	5.615
	NT2RP7003688//	0	//	0.000	//	0.881
30	NT2RP7004114//	0	//	0.000	//	6.650
	NT2RP7004123//	0	//	0.000	//	2.289
	NT2RP7004196//	0	//	0.000	//	1.563
	NT2RP7004348//	0	//	0.000	//	2.695
	NT2RP7004352//	0	//	0.000	//	6.077
35	NT2RP7004373//	0	//	0.000	//	2.807
	NT2RP7004559//	0	//	0.000	//	10.166

	NT2RP7004728//	0	//	0.000	//	1.875
	NT2RP7004751//	0	//	44.129	//	1.116
	NT2RP7004915//	0	//	0.000	//	17.708
	NT2RP7004925//	0	//	0.000	//	1.506
5	NT2RP7004946//	0	//	0.000	//	2.053
	NT2RP7005513//	0	//	0.000	//	2.016
	NT2RP7005529//	0	//	0.000	//	8.806
	NT2RP7005675//	0	//	0.000	//	10.406
	NT2RP7005750//	0	//	0.000	//	4.268
10	NT2RP7006223//	0	//	0.000	//	5.039
	NT2RP7006490//	0	//	0.000	//	2.560
	NT2RP7006539//	0	//	0.000	//	10.410
	NT2RP7006619//	0	//	0.000	//	2.633
	NT2RP7006717//	0	//	0.000	//	5.493
15	NT2RP7006886//	0	//	0.000	//	11.344
	NT2RP7007114//	0	//	0.000	//	19.540
	NT2RP7007154//	0	//	0.000	//	1.360
	NT2RP7007252//	0	//	0.000	//	8.190
	NT2RP7007310//	82.993	//	0	//	0.000
20	NT2RP7007381//	0	//	0.000	//	18.704
	NT2RP7007537//	27.403	//	0	//	0.000
	NT2RP7007610//	0	//	0.000	//	3.452
	NT2RP7008161//	0	//	0.000	//	7.488
	NT2RP7008167//	0	//	0.000	//	2.165
25	NT2RP7008190//	0	//	0.000	//	1.582
	NT2RP7008315//	0	//	0.000	//	8.950
	NT2RP7008543//	0	//	0.000	//	3.281
	NT2RP7009087//	0	//	0.000	//	2.897
	NT2RP7009097//	40.067	//	0	//	0.000
30	NT2RP7009147//	0	//	0.000	//	1.900
	NT2RP7009259//	0	//	0.000	//	2.010
	NT2RP7009482//	0	//	0.000	//	5.527
	NT2RP7010612//	0	//	0.000	//	25.799
	NT2RP7013573//	0	//	0.000	//	8.594
35	NT2RP7017474//	0	//	0.000	//	22.450
	NTONG1000033//	0	//	0.000	//	1.461



	NTONG1000098//	0	//	0.000	//	0.760
	NTONG1000182//	0	//	0.000	//	1.477
	NTONG1000246//	0	//	0.000	//	1.865
	NTONG2000265//	0	//	0.000	//	1.017
5	NTONG2000876//	0	//	0.000	//	1.661
	NTONG2001550//	0	//	0.000	//	4.151
	NTONG2001567//	0	//	0.000	//	1.097
	NTONG2002582//	0	//	0.000	//	13.457
	NTONG2003454//	0	//	0.000	//	24.889
10	NTONG2003839//	0	//	0.000	//	6.254
	NTONG2004844//	0	//	0.000	//	1.933
	NTONG2005363//	0	//	0.000	//	13.929
	NTONG2005391//	0	//	0.000	//	13.902
	NTONG2005520//	0	//	0.000	//	0.794
15	NTONG2005801//	0	//	0.000	//	4.250
	NTONG2005897//	0	//	0.000	//	8.187
	NTONG2008944//	0	//	0.000	//	6.965
	OCBBF1000086//	0	//	0.000	//	1.826
	OCBBF1000175//	0	//	0.000	//	8.591
20	OCBBF2000015//	17.632	//	0	//	3.774
	OCBBF2000467//	0	//	0.000	//	2.406
	OCBBF2000677//	0	//	0.000	//	19.428
	OCBBF2000986//	0	//	0.000	//	1.149
	OCBBF2001166//	0	//	0.000	//	6.537
25	OCBBF2001210//	0	//	0.000	//	4.324
	OCBBF2001323//	0	//	0.000	//	10.255
	OCBBF2001586//	0	//	0.000	//	8.553
	OCBBF2001961//	0	//	0.000	//	48.981
	OCBBF2002086//	0	//	0.000	//	15.370
30	OCBBF2002656//	0	//	0.000	//	1.973
	OCBBF2003246//	0	//	0.000	//	11.672
	OCBBF2003925//	0	//	0.000	//	0.994
	OCBBF2004273//	19.976	//	0	//	0.000
	OCBBF2004757//	0	//	0.000	//	2.956
35	OCBBF2005476//	0	//	0.000	//	16.727
	OCBBF2005956//	0	//	0.000	//	3.386

	OCBBF2006313//	0	//	0.000	//	6.810
	OCBBF2006849//	0	//	0.000	//	2.410
	OCBBF2007028//	0	//	0.000	//	8.234
	OCBBF2007415//	0	//	0.000	//	0.955
5	OCBBF2007829//	0	//	0.000	//	7.203
	OCBBF2008005//	0	//	0.000	//	3.787
	OCBBF2008144//	0	//	0.000	//	3.440
	OCBBF2009242//	0	//	0.000	//	3.377
	OCBBF2009301//	46.196	//	0	//	0.000
10	OCBBF2009424//	0	//	0.000	//	8.655
	OCBBF2009772//	0	//	0.000	//	1.404
	OCBBF2010313//	0	//	0.000	//	16.359
	OCBBF2010557//	0	//	0.000	//	43.708
	OCBBF2010830//	0	//	0.000	//	2.099
15	OCBBF2010945//	0	//	0.000	//	48.981
	OCBBF2011021//	0	//	0.000	//	1.724
	OCBBF2011228//	0	//	0.000	//	25.500
	OCBBF2011232//	0	//	0.000	//	9.556
	OCBBF2011536//	0	//	0.000	//	2.379
20	OCBBF2011759//	0	//	0.000	//	3.344
	OCBBF2013149//	0	//	0.000	//	1.850
	OCBBF2013843//	0	//	50.379	//	0.637
	OCBBF2014064//	0	//	0.000	//	3.258
	OCBBF2014292//	0	//	0.000	//	3.706
25	OCBBF2017398//	0	//	0.000	//	3.068
	OCBBF2017754//	0	//	0.000	//	8.956
	OCBBF2017791//	0	//	0.000	//	9.166
	OCBBF2017882//	0	//	0.000	//	8.510
	OCBBF2018012//	0	//	0.000	//	10.043
30	OCBBF2018563//	0	//	0.000	//	24.528
	OCBBF2018873//	0	//	0.000	//	6.611
	OCBBF2018956//	0	//	0.000	//	2.019
	OCBBF2020741//	0	//	0.000	//	33.655
	OCBBF2021833//	0	//	0.000	//	17.297
35	OCBBF2024850//	0	//	0.000	//	26.505
	OCBBF2026368//	0	//	0.000	//	19.710

	OCBBF2027148//	0	//	0.000	//	27.753
	OCBBF2036743//	0	//	0.000	//	13.183
	OCBBF3001333//	0	//	0.000	//	3.832
	OCBBF3004487//	0	//	0.000	//	5.404
5	PEBLM1000144//	0	//	0.000	//	7.153
	PEBLM2000030//	0	//	0.000	//	4.390
	PEBLM2000147//	0	//	0.000	//	1.522
	PEBLM2000326//	0	//	0.000	//	6.474
	PEBLM2004452//	0	//	0.000	//	6.439
10	PEBLM2006366//	0	//	0.000	//	3.301
	PEBLM2006709//	0	//	0.000	//	6.636
	PERIC2006443//	0	//	0.000	//	5.792
	PERIC2007068//	0	//	0.000	//	5.521
	PLACE5000013//	0	//	0.000	//	9.466
15	PLACE5000113//	0	//	0.000	//	10.260
	PLACE5000159//	0	//	0.000	//	8.132
	PLACE5000170//	0	//	0.000	//	4.147
	PLACE5000372//	0	//	0.000	//	40.126
	PLACE6000145//	23.096	//	0	//	0.000
20	PLACE6000263//	0	//	0.000	//	1.813
	PLACE6000379//	0	//	0.000	//	1.264
	PLACE6000414//	0	//	0.000	//	6.113
	PLACE6001064//	0	//	0.000	//	3.421
	PLACE6001185//	0	//	0.000	//	25.473
25	PLACE6001281//	0	//	0.000	//	4.106
	PLACE6001443//	0	//	0.000	//	11.713
	PLACE6001886//	0	//	0.000	//	40.398
	PLACE6002084//	0	//	0.000	//	0.881
	PLACE6002102//	0	//	0.000	//	6.738
30	PLACE6002668//	0	//	0.000	//	6.437
	PLACE6002960//	0	//	0.000	//	2.647
	PLACE6003218//	0	//	0.000	//	17.355
	PLACE6003383//	0	//	0.000	//	1.424
	PLACE6004005//	0	//	0.000	//	1.178
35	PLACE6004312//	0	//	0.000	//	0.719
	PLACE6004397//	0	//	0.000	//	2.192

	PLACE6004491// 0 // 0.000 // 40.126
	PLACE6004738// 0 // 0.000 // 25.098
	PLACE6005482// 0 // 0.000 // 22.076
	PLACE6006042// 0 // 0.000 // 6.493
5	PLACE6006137// 0 // 0.000 // 4.074
	PLACE6006186// 0 // 0.000 // 25.880
	PLACE6006549// 0 // 0.000 // 1.905
	PLACE6008775// 0 // 0.000 // 6.595
	PLACE6008824// 0 // 0.000 // 40.126
10	PLACE6009338// 0 // 0.000 // 29.967
	PLACE6010077// 0 // 0.000 // 2.077
	PLACE6011057// 0 // 0.000 // 2.688
	PLACE6012942// 0 // 0.000 // 40.126
	PLACE6015731// 0 // 0.000 // 18.307
15	PLACE6016383// 0 // 0.000 // 7.710
	PLACE6017431// 0 // 0.000 // 40.126
	PLACE6018938// 0 // 0.000 // 18.301
	PLACE7006240// 0 // 0.000 // 30.024
	PROST1000097// 0 // 0.000 // 7.013
20	PROST1000199// 16.283 // 0 // 4.357
	PROST1000220// 0 // 0.000 // 0.810
	PROST1000226// 0 // 0.000 // 2.134
	PROST1000246// 0 // 0.000 // 13.104
	PROST1000526// 0 // 0.000 // 3.013
25	PROST1000564// 0 // 0.000 // 1.603
	PROST2000138// 5.795 // 0 // 5.479
	PROST2000273// 0 // 0.000 // 25.167
	PROST2002651// 0 // 0.000 // 7.133
	PROST2003232// 0 // 0.000 // 0.814
30	PROST2003338// 0 // 0.000 // 4.005
	PROST2003396// 0 // 0.000 // 7.125
	PROST2004095// 0 // 0.000 // 1.116
	PROST2004258// 0 // 0.000 // 9.101
	PROST2004270// 0 // 0.000 // 2.104
35	PROST2004416// 0 // 0.000 // 0.811
	PROST2005285// 0 // 0.000 // 8.902

	PROST2005604//	0	//	0.000	//	7.420
	PROST2006030//	0	//	0.000	//	4.513
	PROST2006536//	0	//	0.000	//	2.647
	PROST2006737//	0	//	0.000	//	8.672
5	PROST2007200//	0	//	0.000	//	14.088
	PROST2008271//	0	//	0.000	//	4.674
	PROST2008489//	14.433	//	0	//	0.772
	PROST2008770//	0	//	0.000	//	0.930
	PROST2010318//	0	//	0.000	//	14.395
10	PROST2010545//	0	//	0.000	//	15.696
	PROST2010782//	0	//	0.000	//	0.290
	PROST2012007//	0	//	0.000	//	1.354
	PROST2012448//	0	//	0.000	//	9.731
	PROST2012890//	0	//	0.000	//	18.191
15	PROST2014916//	0	//	0.000	//	4.345
	PROST2015924//	0	//	0.000	//	8.082
	PROST2016918//	0	//	0.000	//	15.159
	PROST2017203//	0	//	0.000	//	1.549
	PROST2017617//	0	//	0.000	//	25.167
20	PROST2017692//	0	//	0.000	//	0.879
	PROST2018977//	0	//	0.000	//	15.499
	PUAEN1000057//	0	//	0.000	//	7.346
	PUAEN1000065//	0	//	0.000	//	1.598
	PUAEN1000164//	0	//	0.000	//	0.475
25	PUAEN1000239//	0	//	0.000	//	3.697
	PUAEN2000374//	0	//	0.000	//	1.145
	PUAEN2001586//	0	//	0.000	//	3.406
	PUAEN2007044//	0	//	0.000	//	1.710
	PUAEN2008228//	0	//	0.000	//	17.449
30	PUAEN2009655//	0	//	0.000	//	4.359
	SALGL1000157//	0	//	0.000	//	0.465
	SKMUS1000014//	0	//	0.000	//	8.773
	SKMUS1000022//	0	//	0.000	//	0.496
	SKMUS1000084//	0	//	0.000	//	3.674
35	SKMUS1000138//	0	//	0.000	//	0.344
	SKMUS1000177//	0	//	0.000	//	14.082

	SKMUS1000186//	0	//	0.000	//	0.479
	SKMUS2000020//	0	//	0.000	//	4.393
	SKMUS2000343//	0	//	0.000	//	18.379
	SKMUS2000361//	0	//	0.000	//	1.275
5	SKMUS2000380//	0	//	0.000	//	2.586
	SKMUS2000873//	0	//	0.000	//	1.312
	SKMUS2000902//	0	//	0.000	//	12.901
	SKMUS2000931//	0	//	0.000	//	0.649
	SKMUS2000954//	0	//	0.000	//	2.027
10	SKMUS2001129//	0	//	0.000	//	12.130
	SKMUS2001454//	7.522	//	0	//	0.403
	SKMUS2001501//	0	//	0.000	//	2.600
	SKNMC1000110//	0	//	0.000	//	4.318
	SKNMC1000137//	0	//	0.000	//	1.264
15	SKNMC1000168//	0	//	0.000	//	1.997
	SKNMC1000251//	0	//	0.000	//	8.366
	SKNMC2000065//	0	//	0.000	//	2.575
	SKNMC2000097//	0	//	0.000	//	1.063
	SKNMC2000305//	0	//	0.000	//	4.201
20	SKNMC2000635//	0	//	0.000	//	0.856
	SKNMC2000649//	0	//	0.000	//	2.176
	SKNMC2000877//	0	//	0.000	//	2.827
	SKNSH1000086//	0	//	0.000	//	10.184
	SKNSH2000347//	0	//	0.000	//	8.028
25	SKNSH2000482//	0	//	0.000	//	23.251
	SKNSH2000819//	0	//	0.000	//	5.937
	SKNSH2002325//	0	//	0.000	//	4.553
	SKNSH2003528//	0	//	0.000	//	3.621
	SKNSH2008043//	0	//	0.000	//	12.076
30	SMINT1000042//	59.707	//	0	//	6.391
	SMINT1000100//	0	//	0.000	//	6.640
	SMINT1000117//	0	//	0.000	//	1.569
	SMINT1000131//	0	//	0.000	//	3.277
	SMINT2000159//	0	//	0.000	//	6.518
35	SMINT2000277//	0	//	0.000	//	2.162
	SMINT2000396//	0	//	0.000	//	5.840

	SMINT2000441// 0 // 0.000 // 1.615
	SMINT2000468// 0 // 0.000 // 5.458
	SMINT2000545// 0 // 0.000 // 2.827
	SMINT2000629// 0 // 0.000 // 3.203
5	SMINT2001950// 0 // 0.000 // 12.743
	SMINT2002159// 0 // 0.000 // 8.177
	SMINT2002314// 53.944 // 0 // 0.000
	SMINT2002689// 0 // 0.000 // 51.875
	SMINT2002778// 0 // 0.000 // 25.261
10	SMINT2002976// 0 // 0.000 // 6.221
	SMINT2003169// 0 // 0.000 // 0.561
	SMINT2004589// 0 // 0.000 // 4.780
	SMINT2005368// 0 // 0.000 // 1.401
	SMINT2005956// 0 // 0.000 // 6.278
15	SMINT2006801// 0 // 0.000 // 19.209
	SMINT2007187// 0 // 0.000 // 8.007
	SMINT2008960// 0 // 0.000 // 0.816
	SMINT2010959// 0 // 0.000 // 18.459
	SMINT2011033// 0 // 0.000 // 25.261
20	SMINT2012122// 0 // 0.000 // 4.169
	SMINT2013031// 0 // 0.000 // 7.403
	SMINT2013695// 0 // 0.000 // 25.261
	SMINT2014480// 35.406 // 0 // 0.000
	SMINT2018681// 0 // 0.000 // 4.988
25	SPLN1000106// 0 // 0.000 // 13.880
	SPLN1000116// 0 // 0.000 // 0.590
	SPLN1000166// 0 // 0.000 // 2.696
	SPLN2000243// 0 // 0.000 // 25.928
	SPLN2000255// 0 // 0.000 // 5.495
30	SPLN2000505// 0 // 0.000 // 0.503
	SPLN2000839// 0 // 0.000 // 10.886
	SPLN2001141// 0 // 0.000 // 2.253
	SPLN2001157// 0 // 0.000 // 3.280
	SPLN2001689// 0 // 0.000 // 16.646
35	SPLN2002335// 0 // 0.000 // 6.038
	SPLN2002463// 0 // 0.000 // 9.032

	SPLEN2003297//	0	//	0.000	//	31.668
	SPLEN2004220//	0	//	0.000	//	3.430
	SPLEN2005009//	0	//	0.000	//	10.253
	SPLEN2005429//	0	//	0.000	//	17.478
5	SPLEN2005927//	0	//	0.000	//	5.136
	SPLEN2006122//	18.769	//	0	//	0.000
	SPLEN2006133//	21.141	//	0	//	2.263
	SPLEN2006143//	0	//	0.000	//	2.668
	SPLEN2006232//	0	//	0.000	//	3.421
10	SPLEN2006305//	0	//	0.000	//	1.507
	SPLEN2006374//	0	//	0.000	//	5.438
	SPLEN2007388//	0	//	0.000	//	31.668
	SPLEN2007498//	0	//	0.000	//	3.121
	SPLEN2009315//	0	//	0.000	//	40.674
15	SPLEN2010195//	0	//	0.000	//	4.164
	SPLEN2011419//	0	//	0.000	//	2.850
	SPLEN2011737//	0	//	0.000	//	3.107
	SPLEN2012571//	0	//	0.000	//	3.792
	SPLEN2012800//	0	//	0.000	//	0.407
20	SPLEN2013690//	0	//	0.000	//	12.880
	SPLEN2014080//	0	//	0.000	//	5.651
	SPLEN2014572//	0	//	0.000	//	7.423
	SPLEN2016268//	9.628	//	0	//	0.000
	SPLEN2016421//	0	//	0.000	//	2.471
25	SPLEN2016554//	0	//	0.000	//	22.228
	SPLEN2016972//	0	//	0.000	//	4.837
	SPLEN2017318//	0	//	0.000	//	6.052
	SPLEN2017918//	0	//	0.000	//	3.262
	SPLEN2018098//	0	//	0.000	//	40.674
30	SPLEN2018157//	0	//	0.000	//	5.754
	SPLEN2019169//	0	//	0.000	//	6.752
	SPLEN2019311//	0	//	0.000	//	57.827
	SPLEN2019405//	0	//	0.000	//	3.416
	SPLEN2021194//	0	//	0.000	//	8.047
35	SPLEN2021273//	0	//	0.000	//	17.589
	SPLEN2022522//	0	//	0.000	//	1.691



	SPLEN2027113//	0	//	0.000	//	1.952
	SPLEN2028466//	0	//	0.000	//	0.987
	SPLEN2031547//	0	//	0.000	//	5.633
	SPLEN2036932//	0	//	0.000	//	3.497
5	SPLEN2039379//	0	//	0.000	//	10.362
	SPLEN2041585//	0	//	0.000	//	40.674
	SPLEN2042714//	0	//	0.000	//	40.674
	STOMA1000186//	0	//	0.000	//	14.912
	STOMA1000189//	0	//	0.000	//	1.865
10	STOMA2000289//	0	//	0.000	//	6.498
	STOMA2000395//	0	//	0.000	//	5.092
	STOMA2000396//	0	//	0.000	//	6.147
	STOMA2002052//	0	//	0.000	//	6.634
	STOMA2004925//	0	//	0.000	//	14.912
15	SYNOV1000124//	0	//	0.000	//	1.327
	SYNOV2001033//	0	//	0.000	//	0.715
	SYNOV2001239//	6.992	//	0	//	0.374
	SYNOV2001262//	0	//	0.000	//	4.977
	SYNOV2017055//	0	//	0.000	//	20.136
20	SYNOV4000598//	0	//	0.000	//	35.608
	SYNOV4001224//	0	//	0.000	//	35.608
	SYNOV4001395//	0	//	0.000	//	21.660
	SYNOV4009575//	0	//	0.000	//	5.715
	T1ESE2000904//	0	//	0.000	//	2.754
25	TBAES2000059//	0	//	0.000	//	1.797
	TBAES2003702//	0	//	0.000	//	14.497
	TBAES2009387//	0	//	0.000	//	0.638
	TCERX2000613//	0	//	0.000	//	14.497
	TESOP2002273//	0	//	0.000	//	4.841
30	TESOP2006893//	0	//	0.000	//	10.246
	TESTI1000023//	0	//	0.000	//	2.000
	TESTI2000184//	0	//	0.000	//	4.045
	TESTI2000356//	0	//	0.000	//	20.914
	TESTI2000784//	0	//	0.000	//	5.421
35	TESTI2000970//	0	//	0.000	//	5.798
	TESTI2001099//	0	//	0.000	//	4.091

	TESTI2001153//	0	//	0.000	//	5.699
	TESTI2001420//	0	//	0.000	//	64.596
	TESTI2001829//	0	//	0.000	//	1.013
	TESTI2001862//	0	//	0.000	//	3.154
5	TESTI2002149//	0	//	0.000	//	3.990
	TESTI2002365//	0	//	0.000	//	3.907
	TESTI2002632//	0	//	0.000	//	12.913
	TESTI2002877//	0	//	0.000	//	44.500
	TESTI2003005//	0	//	0.000	//	3.623
10	TESTI2003533//	0	//	0.000	//	1.034
	TESTI2004031//	8.934	//	0	//	0.478
	TESTI2004295//	0	//	0.000	//	9.766
	TESTI2004737//	0	//	0.000	//	2.113
	TESTI2004929//	0	//	0.000	//	3.386
15	TESTI2005731//	0	//	0.000	//	3.941
	TESTI2005759//	0	//	0.000	//	2.231
	TESTI2005908//	0	//	0.000	//	1.878
	TESTI2006051//	0	//	0.000	//	0.505
	TESTI2006111//	0	//	0.000	//	24.590
20	TESTI2006588//	0	//	0.000	//	4.520
	TESTI2007211//	0	//	0.000	//	3.939
	TESTI2007407//	0	//	0.000	//	7.322
	TESTI2008240//	0	//	0.000	//	2.982
	TESTI2008835//	0	//	0.000	//	12.941
25	TESTI2009520//	0	//	0.000	//	0.894
	TESTI2009577//	0	//	0.000	//	2.108
	TESTI2009785//	0	//	0.000	//	6.845
	TESTI2010513//	8.756	//	0	//	1.874
	TESTI2011683//	0	//	0.000	//	38.615
30	TESTI2014838//	0	//	0.000	//	3.160
	TESTI2015213//	0	//	0.000	//	0.612
	TESTI2015626//	7.329	//	0	//	0.784
	TESTI2017954//	0	//	0.000	//	0.790
	TESTI2018462//	0	//	0.000	//	3.370
35	TESTI2020871//	0	//	0.000	//	64.596
	TESTI2021124//	0	//	0.000	//	6.816

TESTI2021358// 0 // 0.000 // 40.357  
TESTI2021425// 0 // 0.000 // 4.107  
TESTI2027165// 0 // 0.000 // 64.596  
TESTI2029259// 73.757 // 0 // 3.947  
5 TESTI2033441// 0 // 0.000 // 2.618  
TESTI2034940// 0 // 0.000 // 1.864  
TESTI2036913// 0 // 0.000 // 24.204  
TESTI2036969// 0 // 0.000 // 4.285  
TESTI2039177// 0 // 0.000 // 4.943  
10 TESTI2044788// 0 // 0.000 // 64.596  
TESTI2046456// 0 // 0.000 // 1.104  
TESTI2047605// 0 // 0.000 // 17.379  
TESTI2053723// 0 // 0.000 // 5.399  
TESTI4000014// 0 // 0.000 // 0.639  
15 TESTI4001467// 0 // 0.000 // 6.603  
TESTI4002072// 0 // 0.000 // 3.983  
TESTI4002195// 0 // 0.000 // 15.959  
TESTI4002799// 9.842 // 0 // 1.053  
TESTI4003703// 0 // 0.000 // 5.277  
20 TESTI4003944// 0 // 0.000 // 41.606  
TESTI4005399// 0 // 0.000 // 9.300  
TESTI4005534// 0 // 0.000 // 33.259  
TESTI4008797// 0 // 0.000 // 14.824  
TESTI4009286// 0 // 0.000 // 2.594  
25 TESTI4013441// 0 // 14.788 // 0.374  
TESTI4013675// 0 // 0.000 // 35.326  
TESTI4013894// 0 // 0.000 // 33.408  
TESTI4014159// 0 // 0.000 // 13.979  
TESTI4018886// 0 // 0.000 // 64.596  
30 TESTI4024245// 0 // 0.000 // 40.205  
TESTI4029671// 0 // 0.000 // 22.183  
TESTI4037156// 0 // 0.000 // 1.320  
TESTI4038284// 41.043 // 0 // 0.000  
THYMU1000002// 13.191 // 0 // 0.000  
35 THYMU1000016// 0 // 0.000 // 2.304  
THYMU1000041// 0 // 0.000 // 5.672

	THYMU1000083// 0 // 0.000 // 10.729
	THYMU1000103// 0 // 0.000 // 2.103
	THYMU1000109// 0 // 0.000 // 0.939
	THYMU1000142// 0 // 0.000 // 58.853
5	THYMU1000316// 0 // 0.000 // 58.853
	THYMU1000359// 0 // 0.000 // 1.918
	THYMU1000374// 0 // 0.000 // 3.573
	THYMU1000394// 0 // 0.000 // 11.726
	THYMU1000428// 0 // 0.000 // 0.678
10	THYMU2000382// 0 // 0.000 // 2.892
	THYMU2000436// 20.534 // 0 // 1.099
	THYMU2000684// 0 // 0.000 // 4.966
	THYMU2001007// 0 // 0.000 // -6.471
	THYMU2001422// 0 // 0.000 // 14.855
15	THYMU2002583// 0 // 0.000 // 0.618
	THYMU2002815// 0 // 0.000 // 39.408
	THYMU2003012// 0 // 0.000 // 2.090
	THYMU2003046// 0 // 0.000 // 4.585
	THYMU2003419// 0 // 0.000 // 3.594
20	THYMU2003446// 0 // 0.000 // 2.845
	THYMU2003891// 0 // 0.000 // 0.174
	THYMU2003981// 0 // 0.000 // 2.491
	THYMU2004152// 0 // 0.000 // 1.184
	THYMU2004410// 0 // 0.000 // 2.285
25	THYMU2005546// 12.190 // 0 // 0.000
	THYMU2006505// 0 // 0.000 // 6.513
	THYMU2006813// 0 // 0.000 // 1.887
	THYMU2007415// 0 // 0.000 // 8.658
	THYMU2007467// 0 // 0.000 // 4.818
30	THYMU2007886// 30.859 // 0 // 0.000
	THYMU2008686// 0 // 0.000 // 14.535
	THYMU2008725// 0 // 0.000 // 15.552
	THYMU2009658// 0 // 0.000 // 0.418
	THYMU2010094// 0 // 0.000 // 6.947
35	THYMU2010448// 0 // 0.000 // 6.315
	THYMU2012024// 0 // 0.000 // 3.554

	THYMU2013916//	0	//	0.000	//	2.646
	THYMU2015321//	0	//	0.000	//	58.853
	THYMU2019021//	0	//	0.000	//	5.796
	THYMU2020667//	0	//	0.000	//	41.697
5	THYMU2021684//	0	//	0.000	//	58.853
	THYMU2024071//	0	//	0.000	//	39.309
	THYMU2025319//	0	//	0.000	//	39.408
	THYMU2031890//	0	//	0.000	//	21.176
	THYMU2033070//	0	//	0.000	//	58.853
10	THYMU2034917//	0	//	0.000	//	23.175
	THYMU2035735//	0	//	0.000	//	11.014
	THYMU2036461//	0	//	0.000	//	18.090
	THYMU3001472//	0	//	0.000	//	20.097
	THYMU3002578//	0	//	0.000	//	36.487
15	THYMU3013386//	0	//	0.000	//	1.786
	THYMU3021586//	0	//	0.000	//	4.926
	THYMU3026350//	0	//	0.000	//	17.045
	THYMU3028410//	0	//	0.000	//	58.853
	THYMU3032798//	0	//	0.000	//	2.306
20	THYMU3034616//	0	//	0.000	//	58.853
	THYMU3034671//	0	//	0.000	//	19.911
	TOVAR2000476//	50.572	//	0	//	0.000
	TRACH1000030//	0	//	0.000	//	5.760
	TRACH1000038//	0	//	0.000	//	8.984
25	TRACH1000063//	0	//	0.000	//	2.565
	TRACH1000181//	0	//	0.000	//	5.650
	TRACH1000205//	0	//	0.000	//	4.694
	TRACH2000079//	0	//	0.000	//	0.646
	TRACH2000237//	0	//	0.000	//	6.412
30	TRACH2000248//	0	//	0.000	//	2.496
	TRACH2000321//	0	//	0.000	//	2.344
	TRACH2000359//	0	//	0.000	//	3.557
	TRACH2000461//	0	//	0.000	//	2.045
	TRACH2000472//	0	//	0.000	//	9.166
35	TRACH2000780//	0	//	0.000	//	5.212
	TRACH2000959//	0	//	0.000	//	0.582

	TRACH2001021// 9.332 // 0 // 1.498
	TRACH2001192// 0 // 0.000 // 40.205
	TRACH2001289// 0 // 0.000 // 1.622
	TRACH2001432// 0 // 0.000 // 1.327
5	TRACH2001443// 0 // 0.000 // 11.083
	TRACH2001463// 0 // 0.000 // 3.652
	TRACH2001549// 0 // 0.000 // 5.043
	TRACH2001596// 0 // 0.000 // 24.409
	TRACH2001612// 0 // 0.000 // 4.764
10	TRACH2001810// 0 // 0.000 // 0.926
	TRACH2002054// 0 // 0.000 // 51.568
	TRACH2002537// 0 // 0.000 // 2.212
	TRACH2003272// 0 // 0.000 // 4.419
	TRACH2003323// 0 // 0.000 // 2.123
15	TRACH2005811// 0 // 0.000 // 1.258
	TRACH2007399// 0 // 0.000 // 1.685
	TRACH2008300// 0 // 0.000 // 2.025
	TRACH2014124// 0 // 0.000 // 3.693
	TRACH2014442// 50.173 // 0 // 0.000
20	TRACH2014997// 0 // 0.000 // 25.316
	TRACH2015823// 0 // 0.000 // 5.218
	TRACH2016481// 0 // 0.000 // 51.568
	TRACH2017609// 0 // 0.000 // 37.903
	TRACH2018950// 0 // 0.000 // 17.915
25	TRACH3000692// 0 // 0.000 // 5.590
	TRACH3002192// 0 // 0.000 // 4.463
	TRACH3003379// 0 // 0.000 // 29.185
	TRACH3003547// 0 // 0.000 // 5.044
	TRACH3003872// 0 // 0.000 // 9.820
30	TRACH3004068// 0 // 0.000 // 1.700
	TRACH3004721// 0 // 0.000 // 3.467
	TRACH3005699// 0 // 0.000 // 22.893
	TRACH3006800// 0 // 0.000 // 34.742
	TRACH3007479// 0 // 0.000 // 3.848
35	TRACH3008632// 0 // 0.000 // 20.157
	TRACH3009008// 0 // 0.000 // 5.843

	TRACH3009148//	0	//	0.000	//	10.698
	TUTER1000014//	100.000	//	0	//	0.000
	TUTER1000122//	72.738	//	0	//	0.000
	TUTER1000137//	95.706	//	0	//	0.000
5	TUTER2000057//	92.461	//	0	//	0.000
	TUTER2000283//	100.000	//	0	//	0.000
	TUTER2000425//	100.000	//	0	//	0.000
	TUTER2000904//	62.217	//	0	//	3.330
	TUTER2000916//	100.000	//	0	//	0.000
10	TUTER2001286//	100.000	//	0	//	0.000
	TUTER2001341//	100.000	//	0	//	0.000
	TUTER2001387//	100.000	//	0	//	0.000
	TUTER2001433//	100.000	//	0	//	0.000
	TUTER2001461//	100.000	//	0	//	0.000
15	TUTER2002028//	100.000	//	0	//	0.000
	TUTER2002074//	100.000	//	0	//	0.000
	TUTER2002158//	100.000	//	0	//	0.000
	TUTER2002228//	100.000	//	0	//	0.000
	TUTER2002323//	72.582	//	0	//	0.000
20	TUTER2002356//	100.000	//	0	//	0.000
	TUTER2002729//	100.000	//	0	//	0.000
	UMVEN1000122//	0	//	92.143	//	0.000
	UMVEN1000143//	0	//	77.431	//	0.000
	UMVEN1000156//	0	//	97.424	//	0.000
25	UMVEN1000186//	0	//	74.732	//	0.630
	UMVEN2000046//	0	//	100.000	//	0.000
	UMVEN2000069//	0	//	100.000	//	0.000
	UMVEN2000121//	0	//	97.690	//	0.000
	UMVEN2000133//	0	//	55.263	//	2.097
30	UMVEN2000152//	0	//	74.264	//	0.000
	UMVEN2000354//	0	//	77.661	//	0.000
	UMVEN2000453//	0	//	49.229	//	1.245
	UTERU1000000//	0	//	0.000	//	58.°53
	UTERU1000015//	0	//	0.000	//	100.000
35	UTERU1000024//	0	//	0.000	//	100.000
	UTERU1000031//	0	//	0.000	//	100.000

	UTERU1000032// 0 // 0.000 // 100.000
	UTERU1000057// 0 // 0.000 // 100.000
	UTERU1000065// 0 // 0.000 // 100.000
	UTERU1000077// 0 // 0.000 // 100.000
5	UTERU1000093// 0 // 0.000 // 100.000
	UTERU1000096// 0 // 0.000 // 24.268
	UTERU1000106// 0 // 0.000 // 6.873
	UTERU1000109// 0 // 0.000 // 100.000
	UTERU1000131// 0 // 0.000 // 100.000
10	UTERU1000138// 0 // 0.000 // 100.000
	UTERU1000148// 0 // 0.000 // 100.000
	UTERU1000160// 0 // 0.000 // 100.000
	UTERU1000182// 0 // 0.000 // 1.935
	UTERU1000183// 0 // 0.000 // 100.000
15	UTERU1000187// 0 // 0.000 // 100.000
	UTERU1000192// 0 // 0.000 // 100.000
	UTERU1000249// 0 // 0.000 // 100.000
	UTERU1000337// 0 // 0.000 // 100.000
	UTERU1000339// 0 // 0.000 // 100.000
20	UTERU1000384// 0 // 0.000 // 8.500
	UTERU2000023// 0 // 0.000 // 24.419
	UTERU2000047// 0 // 0.000 // 100.000
	UTERU2000074// 0 // 0.000 // 62.692
	UTERU2000095// 0 // 0.000 // 0.987
25	UTERU2000099// 0 // 0.000 // 100.000
	UTERU2000154// 0 // 0.000 // 100.000
	UTERU2000197// 0 // 0.000 // 39.231
	UTERU2000218// 0 // 0.000 // 100.000
	UTERU2000238// 0 // 0.000 // 100.000
30	UTERU2000243// 0 // 0.000 // 100.000
	UTERU2000260// 0 // 0.000 // 24.831
	UTERU2000263// 0 // 0.000 // 2.444
	UTERU2000300// 0 // 0.000 // 11.765
	UTERU2000329// 0 // 0.000 // 68.264
35	UTERU2000332// 0 // 0.000 // 5.640
	UTERU2000338// 0 // 0.000 // 3.979



	UTERU2000349//	0	//	0.000	//	100.000
	UTERU2000377//	0	//	0.000	//	100.000
	UTERU2000393//	0	//	0.000	//	100.000
	UTERU2000418//	0	//	0.000	//	34.205
5	UTERU2000424//	0	//	0.000	//	1.013
	UTERU2000465//	0	//	0.000	//	100.000
	UTERU2000485//	0	//	0.000	//	15.228
	UTERU2000517//	0	//	0.000	//	100.000
	UTERU2000524//	0	//	0.000	//	100.000
10	UTERU2000537//	0	//	0.000	//	12.239
	UTERU2000539//	0	//	0.000	//	100.000
	UTERU2000541//	0	//	0.000	//	7.522
	UTERU2000542//	0	//	0.000	//	-10.769
	UTERU2000546//	0	//	0.000	//	100.000
15	UTERU2000550//	0	//	0.000	//	100.000
	UTERU2000569//	0	//	0.000	//	100.000
	UTERU2000607//	0	//	0.000	//	100.000
	UTERU2000629//	0	//	0.000	//	100.000
	UTERU2000649//	0	//	0.000	//	100.000
20	UTERU2000663//	0	//	0.000	//	100.000
	UTERU2000696//	63.416	//	0	//	3.394
	UTERU2000794//	0	//	0.000	//	100.000
	UTERU2000830//	0	//	0.000	//	100.000
	UTERU2000844//	0	//	0.000	//	100.000
25	UTERU2000922//	0	//	0.000	//	100.000
	UTERU2000925//	0	//	0.000	//	12.420
	UTERU2001024//	0	//	0.000	//	100.000
	UTERU2001110//	0	//	0.000	//	24.268
	UTERU2001176//	0	//	0.000	//	100.000
30	UTERU2001281//	0	//	0.000	//	100.000
	UTERU2001389//	0	//	0.000	//	100.000
	UTERU2001409//	0	//	0.000	//	100.000
	UTERU2001412//	0	//	0.000	//	100.000
	UTERU2001504//	0	//	0.000	//	100.000
35	UTERU2001607//	0	//	0.000	//	1.759
	UTERU2001658//	0	//	0.000	//	10.564

	UTERU2001747//	0	//	0.000	//	100.000
	UTERU2001876//	0	//	0.000	//	100.000
	UTERU2002001//	0	//	0.000	//	40.126
	UTERU2002011//	0	//	0.000	//	100.000
5	UTERU2002176//	0	//	0.000	//	100.000
	UTERU2002198//	0	//	0.000	//	64.596
	UTERU2002294//	0	//	0.000	//	2.165
	UTERU2002332//	0	//	0.000	//	100.000
	UTERU2002410//	13.085	//	0	//	0.700
10	UTERU2002473//	0	//	0.000	//	100.000
	UTERU2002547//	0	//	0.000	//	100.000
	UTERU2002662//	0	//	0.000	//	4.244
	UTERU2002693//	0	//	0.000	//	100.000
	UTERU2002733//	0	//	0.000	//	100.000
15	UTERU2002736//	0	//	0.000	//	100.000
	UTERU2002737//	0	//	0.000	//	100.000
	UTERU2002826//	82.260	//	0	//	4.402
	UTERU2002841//	0	//	0.000	//	64.596
	UTERU2002964//	0	//	0.000	//	25.187
20	UTERU2002993//	0	//	0.000	//	64.596
	UTERU2003035//	0	//	0.000	//	100.000
	UTERU2003057//	0	//	0.000	//	3.085
	UTERU2003126//	0	//	0.000	//	100.000
	UTERU2003135//	0	//	0.000	//	100.000
25	UTERU2003321//	0	//	0.000	//	47.706
	UTERU2003399//	0	//	0.000	//	100.000
	UTERU2003411//	0	//	0.000	//	0.360
	UTERU2003456//	0	//	0.000	//	12.899
	UTERU2003577//	0	//	0.000	//	100.000
30	UTERU2003704//	0	//	0.000	//	20.529
	UTERU2003926//	0	//	0.000	//	40.126
	UTERU2003973//	0	//	0.000	//	100.000
	UTERU2004015//	0	//	0.000	//	100.000
	UTERU2004037//	0	//	0.000	//	5.230
35	UTERU2004039//	0	//	0.000	//	100.000
	UTERU2004061//	0	//	0.000	//	100.000

	UTERU2004073// 0 // 0.000 // 23.318
	UTERU2004163// 0 // 0.000 // 100.000
	UTERU2004197// 0 // 0.000 // 4.796
	UTERU2004299// 0 // 0.000 // 100.000
5	UTERU2004461// 0 // 0.000 // 32.361
	UTERU2004520// 0 // 0.000 // 39.037
	UTERU2004564// 0 // 0.000 // 100.000
	UTERU2004664// 0 // 0.000 // 4.048
	UTERU2004688// 0 // 0.000 // 6.630
10	UTERU2004698// 0 // 0.000 // 100.000
	UTERU2004807// 0 // 0.000 // 17.972
	UTERU2004861// 0 // 0.000 // 56.434
	UTERU2004929// 0 // 0.000 // 13.845
	UTERU2005004// 0 // 0.000 // 41.697
15	UTERU2005050// 0 // 0.000 // 100.000
	UTERU2005069// 0 // 0.000 // 64.596
	UTERU2005074// 0 // 0.000 // 27.087
	UTERU2005179// 0 // 0.000 // 100.000
	UTERU2005292// 0 // 0.000 // 3.714
20	UTERU2005346// 0 // 0.000 // 100.000
	UTERU2005354// 0 // 0.000 // 2.609
	UTERU2005446// 0 // 0.000 // 24.816
	UTERU2005449// 0 // 0.000 // 19.526
	UTERU2005450// 0 // 0.000 // 100.000
25	UTERU2005533// 0 // 0.000 // 100.000
	UTERU2005593// 0 // 0.000 // 4.016
	UTERU2005601// 0 // 0.000 // 3.040
	UTERU2005621// 0 // 0.000 // 5.377
	UTERU2005664// 0 // 0.000 // 13.328
30	UTERU2005822// 0 // 0.000 // 100.000
	UTERU2005903// 0 // 0.000 // 100.000
	UTERU2005905// 0 // 0.000 // 100.000
	UTERU2006103// 0 // 0.000 // 100.000
	UTERU2006115// 0 // 0.000 // 9.347
35	UTERU2006137// 0 // 0.000 // 9.269
	UTERU2006182// 0 // 0.000 // 100.000

	UTERU2006400//	0	//	0.000	//	15.228
	UTERU2006412//	0	//	0.000	//	100.000
	UTERU2006429//	0	//	0.000	//	100.000
	UTERU2006486//	0	//	0.000	//	51.819
5	UTERU2006524//	0	//	0.000	//	53.896
	UTERU2006547//	0	//	0.000	//	24.268
	UTERU2006568//	0	//	0.000	//	100.000
	UTERU2006593//	0	//	0.000	//	3.522
	UTERU2006643//	0	//	0.000	//	10.128
10	UTERU2006651//	0	//	0.000	//	100.000
	UTERU2006705//	0	//	0.000	//	100.000
	UTERU2006899//	0	//	0.000	//	100.000
	UTERU2007004//	0	//	0.000	//	24.856
	UTERU2007075//	0	//	0.000	//	100.000
15	UTERU2007081//	0	//	0.000	//	17.449
	UTERU2007128//	0	//	0.000	//	100.000
	UTERU2007253//	0	//	0.000	//	12.290
	UTERU2007267//	0	//	0.000	//	100.000
	UTERU2007444//	0	//	0.000	//	64.596
20	UTERU2007499//	0	//	0.000	//	100.000
	UTERU2007639//	0	//	0.000	//	100.000
	UTERU2007724//	0	//	0.000	//	15.672
	UTERU2007924//	0	//	0.000	//	3.190
	UTERU2007942//	0	//	0.000	//	100.000
25	UTERU2008018//	0	//	0.000	//	24.856
	UTERU2008019//	0	//	0.000	//	100.000
	UTERU2008027//	0	//	0.000	//	4.562
	UTERU2008040//	0	//	0.000	//	14.037
	UTERU2008077//	0	//	0.000	//	100.000
30	UTERU2008085//	0	//	0.000	//	0.323
	UTERU2008130//	0	//	0.000	//	53.896
	UTERU2008302//	0	//	0.000	//	3.187
	UTERU2008347//	0	//	0.000	//	100.000
	UTERU2008426//	0	//	0.000	//	26.260
35	UTERU2008516//	0	//	0.000	//	100.000
	UTERU2008561//	0	//	0.000	//	100.000

	UTERU2008653//	0	//	0.000	//	48.981
	UTERU2008705//	0	//	0.000	//	100.000
	UTERU2008707//	0	//	0.000	//	100.000
	UTERU2008747//	0	//	0.000	//	10.541
5	UTERU2008785//	0	//	0.000	//	100.000
	UTERU2008845//	0	//	0.000	//	100.000
	UTERU2008901//	0	//	0.000	//	100.000
	UTERU2008930//	0	//	0.000	//	100.000
	UTERU2008938//	0	//	0.000	//	8.806
10	UTERU2008939//	0	//	0.000	//	17.716
	UTERU2008962//	0	//	0.000	//	64.596
	UTERU2009094//	0	//	0.000	//	100.000
	UTERU2009120//	0	//	0.000	//	100.000
	UTERU2009131//	0	//	0.000	//	100.000
15	UTERU2009147//	0	//	0.000	//	100.000
	UTERU2009206//	0	//	0.000	//	100.000
	UTERU2009283//	0	//	0.000	//	100.000
	UTERU2009335//	0	//	0.000	//	10.852
	UTERU2009414//	0	//	0.000	//	100.000
20	UTERU2009435//	0	//	0.000	//	12.756
	UTERU2009483//	0	//	0.000	//	100.000
	UTERU2009510//	0	//	0.000	//	17.926
	UTERU2009538//	0	//	0.000	//	40.674
	UTERU2009540//	0	//	0.000	//	100.000
25	UTERU2009776//	0	//	0.000	//	100.000
	UTERU2009904//	0	//	0.000	//	100.000
	UTERU2009951//	0	//	0.000	//	100.000
	UTERU2009972//	0	//	0.000	//	16.901
	UTERU2010115//	0	//	0.000	//	100.000
30	UTERU2010124//	0	//	0.000	//	100.000
	UTERU2010164//	0	//	0.000	//	100.000
	UTERU2010226//	0	//	0.000	//	9.408
	UTERU2010231//	0	//	0.000	//	100.000
	UTERU2010304//	0	//	0.000	//	100.000
35	UTERU2010320//	0	//	0.000	//	25.187
	UTERU2010417//	7.026	//	0	//	1.128

	UTERU2010431// 0 // 0.000 // 100.000
	UTERU2010525// 0 // 0.000 // 14.053
	UTERU2010651// 0 // 0.000 // 100.000
	UTERU2010724// 0 // 0.000 // 100.000
5	UTERU2010747// 0 // 0.000 // 62.692
	UTERU2011195// 0 // 0.000 // 100.000
	UTERU2011199// 0 // 0.000 // 100.000
	UTERU2011220// 0 // 0.000 // 4.669
	UTERU2011261// 0 // 0.000 // 100.000
10	UTERU2011287// 0 // 0.000 // 39.146
	UTERU2011410// 0 // 0.000 // 100.000
	UTERU2011574// 0 // 0.000 // 100.000
	UTERU2011621// 0 // 0.000 // 11.843
	UTERU2011657// 0 // 0.000 // 100.000
15	UTERU2011741// 0 // 0.000 // 14.051
	UTERU2011806// 0 // 0.000 // 49.807
	UTERU2011811// 0 // 0.000 // 100.000
	UTERU2011897// 0 // 0.000 // 100.000
	UTERU2011906// 0 // 0.000 // 16.267
20	UTERU2011962// 0 // 0.000 // 100.000
	UTERU2011968// 0 // 0.000 // 100.000
	UTERU2012031// 0 // 0.000 // 53.896
	UTERU2012101// 0 // 0.000 // 100.000
	UTERU2012114// 0 // 0.000 // 100.000
25	UTERU2012230// 0 // 0.000 // 18.890
	UTERU2012252// 0 // 0.000 // 25.609
	UTERU2012286// 0 // 0.000 // 3.022
	UTERU2012333// 0 // 0.000 // 100.000
	UTERU2012407// 0 // 0.000 // 29.356
30	UTERU2012526// 0 // 0.000 // 11.013
	UTERU2012581// 0 // 0.000 // 100.000
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	UTERU2012615// 0 // 0.000 // 100.000
	UTERU2012688// 0 // 0.000 // 51.568
35	UTERU2012703// 0 // 0.000 // 24.539
	UTERU2012715// 0 // 0.000 // 34.205

	UTERU2012741// 0 // 0.000 // 21.469
	UTERU2012767// 0 // 0.000 // 6.351
	UTERU2012786// 0 // 0.000 // 100.000
	UTERU2012856// 0 // 0.000 // 8.416
5	UTERU2012890// 0 // 0.000 // 100.000
	UTERU2012938// 0 // 0.000 // 48.981
	UTERU2012976// 0 // 0.000 // 100.000
	UTERU2013048// 0 // 0.000 // 100.000
	UTERU2013078// 0 // 0.000 // 16.358
10	UTERU2013231// 0 // 0.000 // 100.000
	UTERU2013262// 0 // 0.000 // 43.775
	UTERU2013280// 0 // 0.000 // 100.000
	UTERU2013322// 0 // 0.000 // 100.000
	UTERU2013483// 0 // 0.000 // 100.000
15	UTERU2013491// 0 // 0.000 // 13.929
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	UTERU2013586// 0 // 0.000 // 7.858
	UTERU2013926// 0 // 0.000 // 100.000
	UTERU2013976// 0 // 0.000 // 100.000
20	UTERU2014001// 0 // 0.000 // 100.000
	UTERU2014024// 0 // 0.000 // 15.457
	UTERU2014167// 0 // 0.000 // 1.087
	UTERU2014223// 0 // 0.000 // 100.000
	UTERU2014398// 0 // 0.000 // 100.000
25	UTERU2014464// 0 // 0.000 // 16.101
	UTERU2014548// 0 // 0.000 // 39.231
	UTERU2014601// 0 // 0.000 // 16.520
	UTERU2014631// 0 // 0.000 // 100.000
	UTERU2014668// 0 // 0.000 // 39.231
30	UTERU2014678// 0 // 0.000 // 48.981
	UTERU2014728// 0 // 0.000 // 100.000
	UTERU2014898// 0 // 0.000 // 1.815
	UTERU2014998// 0 // 0.000 // 100.000
	UTERU2015062// 0 // 0.000 // 17.070
35	UTERU2015087// 0 // 0.000 // 100.000
	UTERU2015108// 0 // 0.000 // 7.526

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	UTERU2015198//	0	//	0.000	//	100.000
	UTERU2015202//	0	//	0.000	//	100.000
	UTERU2015405//	0	//	0.000	//	100.000
5	UTERU2015640//	0	//	0.000	//	100.000
	UTERU2015653//	0	//	0.000	//	4.175
	UTERU2015830//	0	//	0.000	//	58.853
	UTERU2015880//	0	//	0.000	//	100.000
	UTERU2016147//	0	//	0.000	//	100.000
10	UTERU2016157//	0	//	0.000	//	100.000
	UTERU2016426//	0	//	0.000	//	15.158
	UTERU2016464//	0	//	0.000	//	100.000
	UTERU2016669//	0	//	0.000	//	9.848
	UTERU2016757//	0	//	0.000	//	54.394
15	UTERU2016761//	0	//	0.000	//	100.000
	UTERU2016799//	0	//	0.000	//	10.404
	UTERU2016822//	0	//	0.000	//	19.178
	UTERU2016896//	0	//	0.000	//	100.000
	UTERU2016902//	0	//	0.000	//	100.000
20	UTERU2016979//	0	//	0.000	//	12.336
	UTERU2016981//	0	//	0.000	//	100.000
	UTERU2017123//	0	//	0.000	//	100.000
	UTERU2017303//	0	//	0.000	//	100.000
	UTERU2017421//	0	//	0.000	//	100.000
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	UTERU2017613//	0	//	0.000	//	12.264
	UTERU2017623//	0	//	0.000	//	64.596
	UTERU2017632//	0	//	0.000	//	64.596
	UTERU2017761//	0	//	0.000	//	62.692
30	UTERU2017762//	0	//	0.000	//	39.037
	UTERU2017810//	0	//	0.000	//	100.000
	UTERU2017988//	0	//	0.000	//	100.000
	UTERU2018127//	0	//	0.000	//	100.000
	UTERU2018180//	0	//	0.000	//	100.000
35	UTERU2018200//	0	//	0.000	//	28.946
	UTERU2018333//	0	//	0.000	//	100.000



	UTERU2018364//	0	//	0.000	//	53.896
	UTERU2018514//	0	//	0.000	//	100.000
	UTERU2018522//	0	//	0.000	//	100.000
	UTERU2018523//	0	//	0.000	//	40.126
5	UTERU2018544//	0	//	0.000	//	100.000
	UTERU2018566//	0	//	0.000	//	21.258
	UTERU2018609//	0	//	0.000	//	100.000
	UTERU2018674//	0	//	0.000	//	100.000
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	UTERU2018789//	0	//	0.000	//	100.000
	UTERU2018811//	0	//	0.000	//	100.000
	UTERU2018867//	0	//	0.000	//	100.000
	UTERU2018881//	0	//	0.000	//	100.000
15	UTERU2018884//	0	//	0.000	//	1.848
	UTERU2018955//	0	//	0.000	//	100.000
	UTERU2019005//	0	//	0.000	//	7.703
	UTERU2019038//	0	//	0.000	//	100.000
	UTERU2019096//	0	//	0.000	//	5.495
20	UTERU2019163//	0	//	0.000	//	100.000
	UTERU2019257//	0	//	0.000	//	57.271
	UTERU2019453//	0	//	0.000	//	100.000
	UTERU2019491//	0	//	0.000	//	100.000
	UTERU2019534//	0	//	0.000	//	100.000
25	UTERU2019681//	0	//	0.000	//	100.000
	UTERU2019706//	0	//	0.000	//	54.394
	UTERU2019710//	0	//	0.000	//	100.000
	UTERU2019940//	0	//	0.000	//	51.819
	UTERU2019959//	0	//	0.000	//	100.000
30	UTERU2019964//	0	//	0.000	//	100.000
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	UTERU2020292//	0	//	0.000	//	100.000
	UTERU2020351//	0	//	0.000	//	100.000
35	UTERU2020491//	0	//	0.000	//	100.000
	UTERU2020718//	0	//	0.000	//	100.000

	UTERU2021163// 0 // 0.000 // 53.896
	UTERU2021380// 0 // 0.000 // 100.000
	UTERU2021649// 0 // 0.000 // 100.000
	UTERU2021820// 0 // 0.000 // 29.732
5	UTERU2022020// 0 // 0.000 // 100.000
	UTERU2022773// 0 // 0.000 // 100.000
	UTERU2022955// 0 // 0.000 // 100.000
	UTERU2022981// 0 // 0.000 // 100.000
	UTERU2023039// 0 // 0.000 // 54.394
10	UTERU2023045// 0 // 0.000 // 10.794
	UTERU2023175// 0 // 0.000 // 7.103
	UTERU2023262// 0 // 0.000 // 15.042
	UTERU2023550// 0 // 0.000 // 9.988
	UTERU2023651// 0 // 0.000 // 29.963
15	UTERU2023687// 0 // 0.000 // 100.000
	UTERU2023712// 0 // 0.000 // 100.000
	UTERU2023941// 0 // 0.000 // 100.000
	UTERU2024002// 0 // 0.000 // 100.000
	UTERU2024042// 0 // 0.000 // 100.000
20	UTERU2024141// 0 // 0.000 // 100.000
	UTERU2024481// 0 // 0.000 // 100.000
	UTERU2024656// 0 // 0.000 // 51.568
	UTERU2024758// 0 // 0.000 // 100.000
	UTERU2024820// 0 // 0.000 // 100.000
25	UTERU2024881// 0 // 0.000 // 100.000
	UTERU2024969// 0 // 0.000 // 11.490
	UTERU2025025// 0 // 0.000 // 100.000
	UTERU2025041// 0 // 0.000 // 100.000
	UTERU2025301// 0 // 0.000 // 5.184
30	UTERU2025366// 0 // 0.000 // 100.000
	UTERU2025415// 0 // 0.000 // 100.000
	UTERU2025579// 0 // 0.000 // 100.000
	UTERU2025645// 0 // 0.000 // 100.000
	UTERU2025891// 0 // 0.000 // 100.000
35	UTERU2026025// 0 // 0.000 // 100.000
	UTERU2026090// 0 // 0.000 // 100.000

	UTERU2026142//	0	//	0.000	//	100.000
	UTERU2026203//	0	//	0.000	//	54.394
	UTERU2026775//	0	//	0.000	//	100.000
	UTERU2027023//	0	//	0.000	//	100.000
5	UTERU2027369//	0	//	0.000	//	39.231
	UTERU2027591//	0	//	0.000	//	100.000
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	UTERU2027941//	0	//	0.000	//	100.000
	UTERU2028377//	0	//	0.000	//	100.000
10	UTERU2028734//	0	//	0.000	//	26.183
	UTERU2029503//	0	//	0.000	//	100.000
	UTERU2029660//	0	//	0.000	//	100.000
	UTERU2029742//	0	//	0.000	//	100.000
	UTERU2029953//	0	//	0.000	//	100.000
15	UTERU2030213//	0	//	0.000	//	58.763
	UTERU2030270//	0	//	0.000	//	100.000
	UTERU2030280//	0	//	0.000	//	51.819
	UTERU2031060//	0	//	0.000	//	100.000
	UTERU2031084//	0	//	0.000	//	25.928
20	UTERU2031268//	0	//	0.000	//	100.000
	UTERU2031295//	0	//	0.000	//	100.000
	UTERU2031521//	0	//	0.000	//	100.000
	UTERU2031611//	0	//	0.000	//	100.000
	UTERU2031703//	0	//	0.000	//	100.000
25	UTERU2031834//	0	//	0.000	//	100.000
	UTERU2031851//	0	//	0.000	//	100.000
	UTERU2032075//	0	//	0.000	//	100.000
	UTERU2032220//	0	//	0.000	//	100.000
	UTERU2032279//	0	//	0.000	//	100.000
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	UTERU2033382//	0	//	0.000	//	100.000
	UTERU2033420//	0	//	0.000	//	100.000
35	UTERU2033530//	0	//	0.000	//	100.000
	UTERU2033577//	0	//	0.000	//	100.000

	UTERU2034053//	0	//	0.000	//	100.000
	UTERU2034147//	0	//	0.000	//	58.853
	UTERU2034695//	0	//	0.000	//	100.000
	UTERU2035114//	0	//	0.000	//	51.568
5	UTERU2035187//	0	//	0.000	//	100.000
	UTERU2035231//	0	//	0.000	//	100.000
	UTERU2035306//	0	//	0.000	//	100.000
	UTERU2035323//	0	//	0.000	//	100.000
	UTERU2035328//	0	//	0.000	//	100.000
10	UTERU2035331//	0	//	0.000	//	100.000
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	UTERU2035469//	0	//	0.000	//	100.000
	UTERU2035503//	0	//	0.000	//	100.000
	UTERU2035745//	0	//	0.000	//	100.000
15	UTERU2035908//	0	//	0.000	//	100.000
	UTERU2035926//	0	//	0.000	//	100.000
	UTERU2035978//	0	//	0.000	//	100.000
	UTERU2036089//	0	//	0.000	//	100.000
	UTERU2036347//	0	//	0.000	//	37.903
20	UTERU2036507//	0	//	0.000	//	100.000
	UTERU2036512//	0	//	0.000	//	100.000
	UTERU2036530//	0	//	0.000	//	100.000
	UTERU2036623//	0	//	0.000	//	100.000
	UTERU2036690//	0	//	0.000	//	100.000
25	UTERU2037224//	0	//	0.000	//	100.000
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	UTERU2037423//	0	//	0.000	//	100.000
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	UTERU2037674//	0	//	0.000	//	100.000
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	UTERU2038171//	0	//	0.000	//	100.000
	UTERU2038251//	0	//	0.000	//	100.000
	UTERU3000226//	0	//	0.000	//	62.692
35	UTERU3000298//	0	//	0.000	//	11.036
	UTERU3000402//	0	//	0.000	//	100.000

	UTERU3000645// 0 // 0.000 // 34.742
	UTERU3000665// 0 // 0.000 // 100.000
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	UTERU3000727// 0 // 0.000 // 26.926
5	UTERU3000738// 0 // 0.000 // 41.697
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	UTERU3000899// 0 // 0.000 // 33.654
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	UTERU3001059// 0 // 0.000 // 100.000
	UTERU3001158// 0 // 0.000 // 39.606
	UTERU3001240// 0 // 0.000 // 100.000
15	UTERU3001394// 0 // 0.000 // 100.000
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	UTERU3001558// 0 // 0.000 // 100.000
	UTERU3001571// 0 // 0.000 // 51.819
	UTERU3001585// 0 // 0.000 // 100.000
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	UTERU3001766// 0 // 0.000 // 54.206
	UTERU3001988// 0 // 0.000 // 100.000
	UTERU3002209// 0 // 0.000 // 100.000
25	UTERU3002218// 0 // 0.000 // 51.568
	UTERU3002383// 0 // 0.000 // 100.000
	UTERU3002600// 0 // 0.000 // 100.000
	UTERU3002620// 0 // 0.000 // 100.000
	UTERU3002667// 0 // 0.000 // 100.000
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	UTERU3002731// 0 // 0.000 // 100.000
	UTERU3002768// 0 // 0.000 // 100.000
	UTERU3002786// 0 // 0.000 // 51.568
	UTERU3002993// 0 // 0.000 // 100.000
35	UTERU3003116// 0 // 0.000 // 100.000
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	UTERU3003178//	0	//	0.000	//	100.000
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	UTERU3003495//	0	//	0.000	//	100.000
	UTERU3003523//	0	//	0.000	//	100.000
5	UTERU3003660//	0	//	0.000	//	8.781
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	UTERU3003776//	0	//	0.000	//	100.000
	UTERU3004384//	0	//	0.000	//	53.896
	UTERU3004418//	0	//	0.000	//	34.722
10	UTERU3004477//	0	//	0.000	//	57.271
	UTERU3004523//	0	//	0.000	//	100.000
	UTERU3004616//	0	//	0.000	//	100.000
	UTERU3004635//	0	//	0.000	//	100.000
	UTERU3004709//	0	//	0.000	//	51.819
15	UTERU3004938//	0	//	0.000	//	100.000
	UTERU3004992//	0	//	0.000	//	100.000
	UTERU3005049//	0	//	0.000	//	58.853
	UTERU3005159//	0	//	0.000	//	41.606
	UTERU3005205//	0	//	0.000	//	100.000
20	UTERU3005230//	0	//	0.000	//	58.249
	UTERU3005264//	0	//	0.000	//	100.000
	UTERU3005422//	0	//	0.000	//	25.298
	UTERU3005460//	0	//	0.000	//	62.692
	UTERU3005536//	0	//	0.000	//	62.692
25	UTERU3005585//	0	//	0.000	//	100.000
	UTERU3005767//	26.525	//	0	//	7.098
	UTERU3005907//	0	//	0.000	//	15.610
	UTERU3005970//	0	//	0.000	//	62.692
	UTERU3006008//	0	//	0.000	//	100.000
30	UTERU3006228//	0	//	0.000	//	100.000
	UTERU3006308//	0	//	0.000	//	62.692
	UTERU3006538//	0	//	0.000	//	100.000
	UTERU3006640//	0	//	0.000	//	100.000
	UTERU3006687//	0	//	0.000	//	100.000
35	UTERU3006720//	0	//	0.000	//	100.000
	UTERU3006798//	0	//	0.000	//	100.000

	UTERU3006884// 0 // 0.000 // 100.000
	UTERU3007021// 0 // 0.000 // 34.742
	UTERU3007104// 0 // 0.000 // 51.568
	UTERU3007108// 0 // 0.000 // 100.000
5	UTERU3007134// 0 // 0.000 // 100.000
	UTERU3007419// 0 // 0.000 // 62.692
	UTERU3007640// 0 // 0.000 // 54.394
	UTERU3007731// 0 // 0.000 // 100.000
	UTERU3007913// 0 // 0.000 // 87.049
10	UTERU3008280// 0 // 0.000 // 37.121
	UTERU3008463// 0 // 0.000 // 100.000
	UTERU3008660// 0 // 0.000 // 100.000
	UTERU3008671// 0 // 0.000 // 100.000
	UTERU3008722// 0 // 0.000 // 100.000
15	UTERU3008917// 0 // 0.000 // 100.000
	UTERU3009259// 0 // 0.000 // 53.896
	UTERU3009490// 0 // 0.000 // 100.000
	UTERU3009517// 0 // 0.000 // 54.206
	UTERU3009690// 0 // 0.000 // 100.000
20	UTERU3009775// 0 // 0.000 // 100.000
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Genes whose expression levels were negligibly low in each of the above-described libraries are shown with their clone names below.

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TSTOM2001571, TSTOM2001996, TSTOM2002265, TSTOM2002505,  
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# Homology search data

5 Homology search data for full-length nucleotide sequences and the deduced amino acid sequences are shown below. The search results contain two types of length unit for the sequences compared: aa and bb.

Each piece of data is punctuated with a double slash mark  
10 (//) and shown in order: Sequence Name, Definition of hit data, P value, Length of sequence compared, Homology, and Accession Number of hit data. Sequences which did not show hit data in the homology search list only the Clone name.

3NB692002685// Homo sapiens sperm acrosomal protein mRNA, complete cds.//  
15 7.3E-117// 227aa// 100%// AF047437  
3NB692002806// Dihydropteridine reductase (EC 1.6.99.7) (HDHPR) (Quinoid dihydropteridine reductase).// 1.00E-105// 192aa// 78%// P09417  
3NB692008729  
ACTVT2000380  
20 ADIPS2000088// Human (hybridoma H210) anti-hepatitis A IgG variable region, constant region, complementarity-determining regions mRNA, complete cds.// 3.5E-236// 477aa// 90%// M87789  
ADRGL2000172  
ADRGL2003329  
25 ADRGL2009146  
ADRGL2009691// Mus musculus D111gp1 mRNA, complete cds.// 5.1E-17// 75aa// 60%// AF316996  
ADRGL2009755// Homo sapiens brain and reproductive organ-expressed protein (BRE) mRNA, complete cds.// 2.2E-156// 308aa// 93%// AF015767  
30 ADRGL2012038  
ADRGL2012179  
ASTRO1000009// BAND 4.1-LIKE PROTEIN 4 (NBL4 PROTEIN).// 2.50E-45// 309aa// 38%// 057457  
ASTRO2002842// sentrin/SUMO-specific protease [Mus musculus]// 2.00E-84//  
35 148aa// 54%// NM\_030702  
ASTRO2003960

ASTR02014923// hypothetical protein // 2.6E-66// 133aa// 100%// CAB70760  
 ASTR02018373  
 ASTR03000172  
 ASTR03000177// *Drosophila melanogaster* BcDNA. GH03694 (BcDNA. GH03694) mRNA,  
 5 complete cds.// 1.30E-89// 385aa// 47%// AF181626  
 ASTR03000301// G2 [*Homo sapiens*]// 0// 1073aa// 96%// AAA21253  
 ASTR03000482  
 BLADE1000176  
 BLADE2001371  
 10 BLADE2001987  
 BLADE2002073  
 BLADE2002782// *Rattus norvegicus* clone C53 CDK5 activator-binding protein  
 mRNA, complete cds.// 1.90E-24// 70aa// 82%// AF177476  
 BLADE2002947  
 15 BLADE2003474  
 BLADE2004089// *Mus musculus* PDZ domain actin binding protein Shroom mRNA,  
 complete cds.// 4.20E-244// 784aa// 64%// AF199421  
 BLADE2004462  
 BLADE2004670  
 20 BLADE2005036// CARBOXYPEPTIDASE A1 PRECURSOR (EC 3.4.17.1).// 1.20E-81//  
 168aa// 93%// P15085  
 BLADE2005459  
 BLADE2007666  
 BLADE2007958// *Homo sapiens* U5 snRNP-specific 40 kDa protein mRNA, complete  
 25 cds// 6.0E-91// 190aa// 99%// NP\_004805  
 BLADE2008281  
 BLADE2008398// *Homo sapiens* LRR FLI-1 interacting protein 2 (LRRFIP2) mRNA,  
 complete cds.// 2.00E-98// 200aa// 99%// AF115509  
 BLADE2008539// tumor antigen SLP-8p [*Homo sapiens*]// 0// 427aa// 95%//  
 30 NM\_016516  
 BNGH42003570// *Mus musculus* mRNA for thrombospondin type 1 domain, complete  
 cds.// 2.30E-44// 239aa// 39%// AB016768  
 BNGH420077// VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.// 4.1E-40//  
 242aa// 37%// Q00808  
 35 BRACE1000186// g20 protein [*Homo sapiens*]// 3.00E-74// 138aa// 85%//  
 NM\_016210



BRACE1000258

BRACE1000533

BRACE1000572

BRACE2003639

5 BRACE2005457// PENDRIN.// 1.30E-61// 371aa// 35%// 043511

BRACE2006319// Homo sapiens mRNA for Fln29, complete cds.// 3E-157// 283aa// 99%// AB007447

BRACE2008594// Human protein serine/threonine kinase stk2 mRNA, complete cds.// 1.90E-39// 190aa// 44%// L20321

10 BRACE2010489// Mus musculus nucleolar protein C7 mRNA, complete cds.// 1.70E-149// 391aa// 76%// AF324899

BRACE2011747

BRACE2014306// Chromaffin granule amine transporter--(Vesicular amine transporter 1) (VAT1).// 1.00E-15// 80aa// 22%// P54219

15 BRACE2014475

BRACE2014657

BRACE2015058

BRACE2015314

20 BRACE2016981// Sarcolemmal-associated protein [Homo sapiens]// 7.00E-18// 72aa// 29%// NM\_007159

BRACE2018762// Homer, neuronal immediate early gene, 3 [Homo sapiens]// 1.00E-144// 267aa// 77%// NM\_004838

BRACE2024627

25 BRACE2026836// Mus musculus mRNA for smoothelin L1, large isoform.// 8.00E-66// 220aa// 55%// AJ010305

BRACE2027258// Homo sapiens E2a-Pbx1-associated protein (EB-1) mRNA, partial cds.// 5.80E-163// 302aa// 99%// AF145204

BRACE2027970

BRACE2028970

30 BRACE2029112// Homo sapiens mRNA for plexin-B1 plasma membrane receptor, splice variant R (plexin-B1/SEP gene)// 4.0E-99// 119aa// 62%// AJ011415

BRACE2029849

BRACE2030326// OOCYTE ZINC FINGER PROTEIN XLCOF6 (FRAGMENT).// 1.40E-07// 106aa// 33%// P18749

35 BRACE2030341// Homo sapiens protein kinase STK10 mRNA, partial cds.// 2.60E-66// 129aa// 100%// AF170723

BRACE2030884  
 BRACE2031154  
 BRACE2031389  
 BRACE2031527  
 5 BRACE2031531  
 BRACE2031899  
 BRACE2032044  
 BRACE2032329  
 BRACE2032385  
 10 BRACE2032538  
 BRACE2032823  
 BRACE2033720  
 BRACE2035381// Homo sapiens phospholipase A2, group IVB (cytosolic)  
 (PLA2G4B), mRNA// 0// 446aa// 96%// NM\_005090  
 15 BRACE2035441  
 BRACE2036005  
 BRACE2036096  
 BRACE2036830  
 BRACE2036834  
 20 BRACE2037847  
 BRACE2038114  
 BRACE2038329// Rattus norvegicus CBL-B (Cbl-b) mRNA, partial cds.// 3.4E-96//  
 198aa// 92%// AF199504  
 BRACE2038551// PROTEIN ARGININE N-METHYLTRANSFERASE 2 (EC 2.1.1.-).// 6.40E-  
 25 53// 102aa// 100%// P55345  
 BRACE2039249// POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE (EC 2.4.1.41)  
 (PROTEIN- UDP ACETYL GALACTOSAMINYLTRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N-  
 ACETYL GALACTOSAMINYLTRANSFERASE) (GALNAC-T1).// 5.1E-99// 199aa// 88%//  
 Q10472  
 30 BRACE2039327// hypothetical protein FLJ20241 // 6.3E-47// 97aa// 100%//  
 XP\_012789  
 BRACE2039475  
 BRACE2039734  
 BRACE2040138  
 35 BRACE2040325  
 BRACE2041009

- BRACE2041200// PROTEIN-ARGININE DEIMINASE TYPE II (EC 3.5.3.15)  
(PEPTIDYLARGININE DEIMINASE II) (KIAA0994).// 5.9E-98// 181aa// 98%// Q9Y2J8  
BRACE2041264  
BRACE2042550// Bos taurus mRNA for SCO-spondin, partial.// 1.8E-154// 319aa//  
5 80%// AJ133488  
BRACE2043142  
BRACE2043248// Human I(3)mbt protein homolog mRNA, complete cds.// 7.1E-71//  
140aa// 98%// U89358  
BRACE2043349  
10 BRACE2043665  
BRACE2044286// GUANINE NUCLEOTIDE EXCHANGE FACTOR DBS (DBL'S BIG SISTER)  
(MCF2 TRANSFORMING SEQUENCE-LIKE PROTEIN).// 7.20E-154// 578aa// 50%// Q64096  
BRACE2044816  
BRACE2044949  
15 BRACE2045300// COFILIN, NON-MUSCLE ISOFORM.// 3.9E-85// 166aa// 100%// P23528  
BRACE2045428  
BRACE2045596// CTD-BINDING SR-LIKE PROTEIN RA4 (FRAGMENT).// 1.6E-08//  
160aa// 32%// Q63627  
BRACE2045772// 2-AMINO-3-KETOBUTYRATE COENZYME A LIGASE, MITOCHONDRIAL  
20 PRECURSOR (EC 2.3.1.29) (AKB LIGASE) (GLYCINE ACETYLTRANSFERASE).// 1.3E-  
107// 142aa// 98%// 075600  
BRACE2045947  
BRACE2045954  
BRACE2046251// Homo sapiens hucep-10 mRNA for cerebral protein-10, complete  
25 cds.// 4.3E-135// 264aa// 97%// AB000782  
BRACE2046295// NTAK PROTEIN (NEURAL- AND THYMUS-DERIVED ACTIVATOR FOR ERBB  
KINASES).// 1.80E-165// 304aa// 99%// 014511  
BRACE2047011  
BRACE2047350  
30 BRACE2047377// ras inhibitor [Homo sapiens]// 4.40E-11// 60aa// 58%//  
AAA36553  
BRACE2047385  
BRACE3000071  
BRACE3000697  
35 BRACE3000787

BRACE3000840// Baculoviral IAP repeat-containing protein 1 (Neuronal apoptosis inhibitory protein).// 0// 979aa// 96%// Q13075  
 BRACE3000973  
 BRACE3001002// Zinc finger X-linked protein ZXDB.// 1.00E-45// 97aa// 70%//  
 5 P98169  
 BRACE3001217  
 BRACE3001391// Polycystin precursor (Autosomal dominant polycystic kidney disease protein 1).// 0// 388aa// 84%// P98161  
 BRACE3001595  
 10 BRACE3001754// Surfeit locus protein 5.// 2.00E-87// 166aa// 83%// Q15528  
 BRACE3002298  
 BRACE3002390  
 BRACE3002508// WD40 repeat domain 11 protein [Homo sapiens]// 1.00E-113//  
 200aa// 98%// NM\_018117  
 15 BRACE3003004  
 BRACE3003192// latent transforming growth factor beta binding protein 3 [Homo sapiens]// 0// 670aa// 91%// NM\_021070  
 BRACE3003595// CRK-associated substrate (p130Cas) (Breast cancer anti-estrogen resistance 1 protein).// 0// 712aa// 84%// P56945  
 20 BRACE3003698  
 BRACE3004058// NADH-cytochrome B5 reductase (EC 1.6.2.2) (B5R).// 1.00E-129//  
 220aa// 96%// P00387  
 BRACE3004113  
 BRACE3004150// Heterogeneous nuclear ribonucleoprotein H (hnRNP H).// 0//  
 25 390aa// 86%// P31943  
 BRACE3004358  
 BRACE3004435  
 BRACE3004772// protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 2 [Homo sapiens]// 1.00E-101//  
 30 168aa// 80%// NM\_003625  
 BRACE3004783  
 BRACE3004843  
 BRACE3004^80  
 BRACE3005145  
 35 BRACE3005225  
 BRACE3005430// DNA repair protein rad18.// 4.00E-21// 48aa// 38%// P53692

- BRACE3005499  
 BRACE3006185  
 BRACE3006226  
 BRACE3006462
- 5 BRACE3006872// Echinoderm microtubule-associated protein-like 2 (EMAP-2)  
 (HuEMAP-2).// 1.00E-46// 94aa// 34%// 095834  
 BRACE3007322  
 BRACE3007472  
 BRACE3007480
- 10 BRACE3007559  
 BRACE3007625// espin [Rattus norvegicus]// 1.00E-101// 178aa// 54%//  
 NM\_019622  
 BRACE3007642  
 BRACE3007767
- 15 BRACE3008036  
 BRACE3008092  
 BRACE3008137// Interleukin-16 precursor (IL-16) (Lymphocyte chemoattractant  
 factor) (LCF).// 0// 530aa// 83%// Q14005  
 BRACE3008384// rhomboid (veinlet, Drosophila)-like; Rhomboid, drosophila,  
 20 homolog of [Homo sapiens]// 7.00E-94// 158aa// 51%// NM\_003961  
 BRACE3008720// SP00B-associated GTP-binding protein.// 5.00E-33// 80aa//  
 43%// P20964  
 BRACE3008772  
 BRACE3009090
- 25 BRACE3009237  
 BRACE3009297// mdgl-1 [Mus musculus]// 6.00E-54// 110aa// 84%// AAG17143  
 BRACE3009377  
 BRACE3009574  
 BRACE3009701
- 30 BRACE3009708// Sodium/potassium-transporting ATPase alpha-2 chain precursor  
 (EC 3.6.3.9) (Sodium pump 2) (Na<sup>+</sup>/K<sup>+</sup> ATPase 2).// 0// 868aa// 98%// P50993  
 BRACE3009724  
 BRACE3009747// DAZ associated protein 1 [Homo sapiens]// 2.00E-18// 43aa//  
 57%// NM\_018959
- 35 BRACE3010397// Glioma pathogenesis-related protein (RTVP-1 protein).// 4.00E-  
 29// 65aa// 37%// P48060

BRACE3010428

BRACE3011271// Patched protein homolog 1 (PTC1) (PTC).// 5.00E-84// 147aa//  
72%// Q13635

BRACE3011421// Diacylglycerol kinase, zeta (EC 2.7.1.107) (Diglyceride  
5 kinase) (DGK- zeta) (DAG kinase zeta).// 0// 839aa// 91%// Q13574

BRACE3011505

BRACE3012364

BRACE3012930

BRACE3013119

10 BRACE3013576

BRACE3013740

BRACE3013780

BRACE3014005// thymic stromal cotransporter; putative thymic stromal co-  
transporter TSCOT [Mus musculus]// 4.00E-21// 71aa// 23%// NM\_021053

15 BRACE3014068

BRACE3014231

BRACE3014317

BRACE3014807// homolog 1: tweety homolog [Homo sapiens]// 3.00E-38// 75aa//  
46%// NM\_020659

20 BRACE3015027// Ras GTPase-activating protein nGAP.// 3.00E-75// 214aa// 35%//  
Q9UJF2

BRACE3015121

BRACE3015262// espin [Mus musculus]// 1.00E-10// 55aa// 40%// AAF98134

BRACE3015521// EH-domain containing protein 1 (Testilin) (hPAST1).// 1.00E-  
25 121// 215aa// 93%// Q9H4M9

BRACE3015894

BRACE3016884// Glucoamylase S1/S2 precursor (EC 3.2.1.3) (Glucan 1,4-alpha-  
glucosidase) (1,4-alpha-D-glucan glucohydrolase).// 8.00E-07// 87aa// 17%//  
P08640

30 BRACE3018308

BRACE3018963// Exostosin-like 3 (Putative tumour suppressor protein EXTL3)  
(Multiple exostosis-like protein 3) (Hereditary multiple exostoses gene  
isolog) (EXT-related protein 1).// 6.00E-39// 69aa// 98%// 043909

BRACE3019055

- BRACE3019084// protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 1 [Homo sapiens]// 1.00E-130// 226aa// 93%// NM\_003626
- BRACE3020194
- 5 BRACE3020286
- BRACE3020594// cytokine receptor-like factor 2: cytokine receptor CRL2 precursor [Homo sapiens]// 1.00E-27// 53aa// 73%// NM\_022148
- BRACE3022769
- BRACE3023912
- 10 BRACE3024073// hypothetical protein similar to small G proteins, especially RAP-2A [Homo sapiens]// 8.00E-36// 77aa// 48%// NM\_021183
- BRACE3024659
- BRACE3024662
- BRACE3025153
- 15 BRACE3025457// testis-specific protein TSP-NY [Homo sapiens]// 0// 413aa// 97%// NM\_032573
- BRACE3025531
- BRACE3025630// Alkaline serine exoprotease A precursor (EC 3.4.21.-).// 4.00E-18// 53aa// 33%// P16588
- 20 BRACE3026008
- BRACE3026075
- BRACE3026735
- BRACE3027242
- BRACE3027326// RAP1 GTPase activating protein 1 (RAP1GAP).// 1.00E-177// 331aa// 50%// P47736
- 25 BRACE3027478
- BRACE3030103
- BRACE3031838
- BRACE3032983
- 30 BRACE3040856// Golgi Transport; Got1p [Saccharomyces cerevisiae]// 2.00E-13// 100aa// 45%// NP\_014020
- BRACE3045033// polyamine-modulated factor 1: polyamine modulated factor 1 [Homo sapiens]// 1.00E-41// 82aa// 100%// NM\_007221
- BRALZ2011796
- 35 BRALZ2012183
- BRALZ2012848

- BRALZ2014484
- BRALZ2016085// MONOCARBOXYLATE TRANSPORTER 3 (MCT 3) (RETINAL EPITHELIAL MEMBRANE PROTEIN).// 4.2E-49// 244aa// 33%// Q90632
- BRALZ2016498// Homo sapiens FKSG76 (FKSG76) mRNA, complete cds.// 4.8E-65// 127aa// 99%// AF345564
- 5 BRALZ2017359// Homo sapiens RNA helicase HDB/DICE1 mRNA, partial cds.// 4.4E-62// 318aa// 47%// AF141326
- BRAMY2001473// Rattus norvegicus transmembrane receptor Unc5H2 mRNA, complete cds.// 3.00E-115// 501aa// 44%// U87306
- 10 BRAMY2003008
- BRAMY2004771// CHONDROADHERIN PRECURSOR (CARTILAGE LEUCINE-RICH PROTEIN) (38 KDA BONE PROTEIN).// 2.30E-36// 293aa// 34%// Q27972
- BRAMY2005052// COXSACKIEVIRUS AND ADENOVIRUS RECEPTOR PRECURSOR (COXSACKIEVIRUS B- ADENOVIRUS RECEPTOR) (HCAR) (CVB3 BINDING PROTEIN).// 3.10E-37// 200aa// 35%// P78310
- 15 BRAMY2017528
- BRAMY2019300// CHONDROADHERIN PRECURSOR (CARTILAGE LEUCINE-RICH PROTEIN) (38 KDA BONE PROTEIN).// 8.10E-32// 350aa// 28%// Q27972
- BRAMY2019963
- 20 BRAMY2019985
- BRAMY2020058
- BRAMY2020270
- BRAMY2021498// Mus musculus papilin mRNA, complete cds.// 3E-89// 546aa// 37%// AF314171
- 25 BRAMY2028856
- BRAMY2028914
- BRAMY2029602
- BRAMY2030098
- BRAMY2030109// Homo sapiens hucep-4 mRNA for cerebral protein-4, complete cds.// 7.6E-83// 280aa// 55%// D88259
- 30 BRAMY2030702
- BRAMY2030703
- BRAMY2030799
- BRAMY2031317// Mus musculus semaphorin cytoplasmic domain-associated protein 3A (Semcap3) mRNA, complete cds.// 2.6E-169// 682aa// 50%// AF127084
- 35 BRAMY2031377



BRAMY2031442  
 BRAMY2032014  
 BRAMY2032242  
 BRAMY2032317  
 5 BRAMY2033003// solute carrier family 22 (organic anion transporter), member  
 8 // 5.1E-25// 60aa// 100%// XP\_006015  
 BRAMY2033116  
 BRAMY2033267// Rattus norvegicus mRNA for acetoacetyl-CoA synthetase,  
 complete// 1.7E-42// 148aa// 66%// AB026291  
 10 BRAMY2033594  
 BRAMY2034185  
 BRAMY2034920  
 BRAMY2034993  
 BRAMY2036387  
 15 BRAMY2036396  
 BRAMY2036567// GUANINE NUCLEOTIDE EXCHANGE FACTOR DBS (DBL'S BIG SISTER)  
 (MCF2 TRANSFORMING SEQUENCE-LIKE PROTEIN).// 5.3E-47// 113aa// 83%// Q64096  
 BRAMY2036699  
 BRAMY2036913  
 20 BRAMY2037823  
 BRAMY2038100  
 BRAMY2038484// Homo sapiens MDC-3.13 isoform 2 mRNA, complete cds.// 3.8E-  
 65// 194aa// 60%// AF099935  
 BRAMY2038846  
 25 BRAMY2038904// Homo sapiens mRNA for X-like 1 protein.// 2.7E-199// 738aa//  
 55%// AJ005821  
 BRAMY2039872// Homo sapiens protein phosphatase methylesterase-1 (PME-1) mRNA,  
 complete cds.// 4.1E-43// 84aa// 98%// AF157028  
 BRAMY2040478  
 30 BRAMY2040592// Homo sapiens hucep-11 mRNA for cerebral protein-11, complete  
 cds.// 2.20E-101// 327aa// 64%// AB001596  
 BRAMY2041261  
 BRAMY2041378  
 BRAMY2041542  
 35 BRAMY2042612  
 BRAMY2042641

BRAMY2042760  
 BRAMY2042918  
 BRAMY2044078  
 BRAMY2044246  
 5 BRAMY2045036  
 BRAMY2046478  
 BRAMY2046742  
 BRAMY2046989// Protein bimA.// 4.00E-07// 60aa// 20%// P17885  
 BRAMY2047169  
 10 BRAMY2047420  
 BRAMY2047676  
 BRAMY2047746// nasopharyngeal carcinoma susceptibility protein [Homo sapiens]// 3.00E-18// 50aa// 42%// NM\_013275  
 BRAMY2047751// REGULATOR OF G-PROTEIN SIGNALING 12 (RGS12).// 1.3E-178//  
 15 336aa// 100%// 014924  
 BRAMY2047765  
 BRAMY2047884  
 BRAMY3000206  
 BRAMY3000213// Homo sapiens RaP2 interacting protein 8 (RPIP8) mRNA, complete  
 20 cds.// 5.7E-85// 167aa// 99%// U93871  
 BRAMY3001401  
 BRAMY3001794// Rattus norvegicus Circadian Oscillatory Protein (SCOP) (Scop)// 1.00E-117// 206aa// 59%// NM\_021657  
 BRAMY3002312  
 25 BRAMY3002620  
 BRAMY3002803// p21-activated protein kinase 6 [Homo sapiens]// 0// 598aa// 87%// NM\_020168  
 BRAMY3002805  
 BRAMY3004224  
 30 BRAMY3004672  
 BRAMY3004900  
 BRAMY3004919// Adenylate cyclase, type V (EC 4.6.1.1) (ATP pyrophosphate-lyase) (Adenylyl cyclase).// 0// 831aa// 91%// Q04400  
 BRAMY3005091// Phosphatidylinositol 4-kinase alpha (EC 2.7.1.67) (PI4-kinase)  
 35 (PtdIns-4-kinase) (PI4K-alpha).// 1.00E-111// 192aa// 100%// P42356

BRAMY3005932// Diacylglycerol kinase, zeta (EC 2.7.1.107) (Diglyceride kinase) (DGK- zeta) (DAG kinase zeta) (DGK-IV) (104 kDa diacylglycerol kinase).// 1.00E-35// 71aa// 98%// 008560  
 BRAMY3006297  
 5 BRAMY3007206  
 BRAMY3007609// nuclear RNA export factor 2; TAP like protein 2 [Homo sapiens]// 2.00E-80// 155aa// 60%// NM\_017809  
 BRAMY3008466// kinesin family member 21A [Mus musculus]// 1.00E-167// 277aa// 94%// NM\_016705  
 10 BRAMY3008505  
 BRAMY3008650  
 BRAMY3009811  
 BRAMY3010411  
 BRAMY4000095// ERBB-3 receptor protein-tyrosine kinase precursor (EC 2.7.1.112) (Tyrosine kinase-type cell surface receptor HER3).// 0// 469aa// 80%// P21860  
 15 BRAMY4000229// CORONIN 2A (WD-REPEAT PROTEIN 2) (IR10).// 2.40E-87// 167aa// 71%// Q92828  
 BRAMY4000277// Alpha-1B-glycoprotein.// 1.00E-163// 276aa// 100%// P04217  
 20 BRASW1000053  
 BRASW1000125  
 BRAWH1000127// Mus musculus mRNA for thrombospondin type 1 domain, complete cds.// 8.30E-49// 204aa// 43%// AB016768  
 BRAWH2001395// MYELIN BASIC PROTEIN (MBP).// 7.90E-26// 64aa// 90%// P02686  
 25 BRAWH2001671  
 BRAWH2001940// H.sapiens gene from PAC 1026E2, partial.// 0// 640aa// 98%// AL035289  
 BRAWH2001973  
 BRAWH2002560// deleted in bladder cancer chromosome region candidate 1 [Homo sapiens].// 0// 770aa// 52%// NP\_055433  
 30 BRAWH2002761  
 BRAWH2005315// neuronal-STOP protein // 5.5E-119// 441aa// 56%// CAA75930  
 BRAWH2007658// COXSACKIEVIRUS AND ADENOVIRUS RECEPTOR HOMOLOG PRECURSOR (MCAR).// 8.80E-14// 366aa// 24%// P97792  
 35 BRAWH2010000// golgi autoantigen, golgin subfamily a, 3; golgin-160 [Homo sapiens]// 5.00E-15// 148aa// 23%// NM\_005895

BRAWH2010084  
 BRAWH2010536// paraneoplastic antigen MA1// 5.00E-18// 100aa// 42%//  
 NP\_006020  
 BRAWH2012162// KE03 protein [Homo sapiens]// 2.00E-97// 330aa// 55%//  
 5 AAC17109  
 BRAWH2012326  
 BRAWH2013294  
 BRAWH2013871  
 BRAWH2014414// Cadherin-4 precursor (Retinal-cadherin) (R-cadherin) (R-  
 10 CAD).// 0// 761aa// 90%// P55283  
 BRAWH2014645  
 BRAWH2014662  
 BRAWH2014876  
 BRAWH2014954// Mus musculus neuronal IL-16 mRNA, complete cds.// 4.40E-271//  
 15 604aa// 84%// AF175292  
 BRAWH2016221// T-CELL RECEPTOR BETA CHAIN ANA 11.// 2.90E-07// 80aa// 46%//  
 P06333  
 BRAWH2016439  
 BRAWH2016702  
 20 BRAWH2016724// MAP2=HMW-MAP2 {alternatively spliced} [rats, brain, mRNA  
 Partial, 267 nt].// 3.8E-24// 74aa// 77%// S81002  
 BRAWH3000078// Mus musculus adult male tongue cDNA, RIKEN full-length  
 enriched library, clone:2310010M24, full insert sequence.// 1.20E-29//  
 111aa// 52%// AK009282  
 25 BRAWH3000100// dedicator of cyto-kinesis 1 [Homo sapiens]// 1.00E-10// 67aa//  
 20%// NM\_001380  
 BRAWH3000314  
 BRAWH3000345  
 BRAWH3000491// 40S ribosomal protein S12.// 5.00E-42// 90aa// 84%// P46405  
 30 BRAWH3001326// 5-azacytidine resistance protein azr1.// 4.00E-27// 74aa//  
 31%// Q09189  
 BRAWH3001475  
 BRAWH3001891  
 BRAWH3002574// Calpain 2, large [catalytic] subunit precursor (EC 3.4.22.17)  
 35 (Calcium-activated neutral proteinase) (CANP) (M-type) (M-calpain)  
 (Millimolar-calpain).// 1.00E-84// 156aa// 91%// P17655

BRAWH3002600// cadherin 23; waltzer; otocadherin [Mus musculus]// 3.00E-30//  
 139aa// 28%// NM\_023370  
 BRAWH3002819  
 BRAWH3002821// synaptotagmin-like 2 [Mus musculus]// 0// 358aa// 78%//  
 5 NM\_031394  
 BRAWH3003522  
 BRAWH3003555  
 BRAWH3003727  
 BRAWH3003801  
 10 BRAWH3003992  
 BRAWH3004453  
 BRAWH3004666  
 BRAWH3005132  
 BRAWH3005422  
 15 BRAWH3005912// MIC1 protein. // 1.00E-29// 71aa// 28%// P53258  
 BRAWH3005981  
 BRAWH3006548  
 BRAWH3006792  
 BRAWH3007221  
 20 BRAWH3007506  
 BRAWH3007592  
 BRAWH3007726  
 BRAWH3007783  
 BRAWH3008341// Ubiquitin carboxyl-terminal hydrolase 6 (EC 3.1.2.15)  
 25 (Ubiquitin thiolesterase 6) (Ubiquitin-specific processing protease 6)  
 (Deubiquitinating enzyme 6) (Proto-oncogene TRE-2).// 3.00E-63// 123aa//  
 67%// P35125  
 BRAWH3008634  
 BRAWH3008697  
 30 BRAWH3008931  
 BRAWH3009297  
 BRCAN2002562// Splicing factor, arginine/serine-rich 2 (Splicing factor SC35)  
 (SC-35) (Splicing component, 35 kDa) (PR264 protein).// 6.00E-47// 88aa//  
 88%// Q62093

- BRCAN2002856// AMYLOID BETA A4 PRECURSOR PROTEIN-BINDING FAMILY A MEMBER 2 (NEURON- SPECIFIC X11L PROTEIN) (NEURONAL MUNC18-1-INTERACTING PROTEIN 2) (MINT-2) (ADAPTER PROTEIN X11BETA).// 2.20E-89// 191aa// 93%// Q99767
- 5 BRCAN2002944// Mus musculus huntington yeast partner C (Hypc) mRNA, complete cds.// 2.1E-36// 83aa// 87%// AF135440
- BRCAN2002948// Homo sapiens mRNA for gamma2-adaptin, complete cds.// 6.6E-53// 117aa// 97%// AB015318
- BRCAN2003703// Homo sapiens mRNA for putative serine/threonine protein kinase, partial.// 1.4E-81// 187aa// 89%// AJ006701
- 10 BRCAN2003746// PHOSPHORYLASE B KINASE ALPHA REGULATORY CHAIN, SKELETAL MUSCLE ISOFORM (PHOSPHORYLASE KINASE ALPHA M SUBUNIT).// 5.9E-105// 213aa// 94%// P46020
- BRCAN2003987
- BRCAN2004355
- 15 BRCAN2005436
- BRCAN2006063// COCHLIN PRECURSOR (COCH-5B2).// 5.7E-123// 230aa// 100%// O43405
- BRCAN2006290
- BRCAN2006297
- 20 BRCAN2006450
- BRCAN2007144
- BRCAN2007409
- BRCAN2007426
- BRCAN2008528
- 25 BRCAN2009203// Homo sapiens liprin-alpha2 mRNA, complete cds.// 1.2E-235// 273aa// 93%// AF034799
- BRCAN2009432// hypothetical protein similar to small G proteins, especially RAP-2A [Homo sapiens]// 1.00E-93// 170aa// 92%// NM\_021183
- BRCAN2010376
- 30 BRCAN2011254
- BRCAN2011602
- BRCAN2012355
- BRCAN2012481
- BRCAN2013655
- 35 BRCAN2013660// Arabidopsis thaliana putative protein (F4F15.330) mRNA, complete cds.// 1.1E-24// 138aa// 44%// AF370547

BRCAN2014143  
 BRCAN2014602// DIACYLGLYCEROL KINASE, ZETA (EC 2.7.1.107) (DIGLYCERIDE KINASE) (DGK- ZETA) (DAG KINASE ZETA).// 6.5E-38// 74aa// 94%// Q13574  
 BRCAN2014881  
 5 BRCAN2015371  
 BRCAN2015464  
 BRCAN2016433  
 BRCAN2016619// CRK-associated substrate (p130Cas) (Breast cancer anti-estrogen resistance 1 protein).// 0// 735aa// 84%// P56945  
 10 BRCAN2017442// sarcosine dehydrogenase; dimethylglycine dehydrogenase-like 1. [Homo sapiens]// 5.00E-20// 51aa// 59%// NM\_007101  
 BRCAN2017717  
 BRCAN2017905  
 BRCAN2018935  
 15 BRCAN2019387  
 BRCAN2020710  
 BRCAN2021028  
 BRCAN2024451// REGULATOR OF G-PROTEIN SIGNALING 14 (RGS14) (FRAGMENT).// 1.5E-131// 324aa// 83%// O43566  
 20 BRCAN2024563  
 BRCAN2025712  
 BRCAN2028355// Ca<sup>2+</sup>/calmodulin-dependent protein kinase (EC 2.7.1.123) II gamma-E// 3E-254// 479aa// 98%// J05636  
 BRCOC2000670  
 25 BRCOC2001505// MYELIN BASIC PROTEIN (MBP).// 8.50E-26// 64aa// 90%// P02686  
 BRCOC2003213// Histidyl-tRNA synthetase (EC 6.1.1.21) (Histidine-tRNA ligase) (HisRS).// 0// 421aa// 95%// P12081  
 BRCOC2007034  
 BRCOC2014033  
 30 BRCOC2016525  
 BRCOC2019934  
 BRCOC2020142  
 BRHIP2000691  
 BRHIP2000819// Human mRNA for actin binding protein p57, complete cds.// 1.3E-48// 96aa// 100%// D44497  
 35 BRHIP2000826

BRHIP2000920

BRHIP2001074

BRHIP2001805// Homo sapiens TREK-1 potassium channel (KCNK2) mRNA, complete cds.// 1.8E-49// 134aa// 80%// AF129399

5 BRHIP2001927// Mus musculus mRNA for HS1 binding protein 3.// 2.7E-30// 102aa// 68%// AJ132192

BRHIP2002122// Homo sapiens B aggressive lymphoma long isoform (BAL) mRNA, complete cds.// 1.8E-97// 189aa// 100%// AF307338

10 BRHIP2002172// Mus musculus urea transporter isoform UTA-3 mRNA, complete cds.// 6.9E-208// 452aa// 82%// AF258602

BRHIP2002346

BRHIP2003242

BRHIP2003786// CCA3 [Rattus norvegicus]// 2.60E-199// 603aa// 61%// BAA19969

BRHIP2003917

15 BRHIP2004312

BRHIP2004359// ELAC PROTEIN.// 6.80E-20// 111aa// 37%// Q47012

BRHIP2004814// Homo sapiens gibbon ape leukemia virus receptor 1 (SLC20A1) gene, exon 11 and complete cds.// 1.8E-188// 346aa// 99%// AF102063

BRHIP2004883

20 BRHIP2005236// latrophilin 2 splice variant baaae // 1.3E-203// 250aa// 97%// AAD05305

BRHIP2005354

BRHIP2005600

BRHIP2005719

25 BRHIP2005752// NG5 [Homo sapiens]// 5.0E-61// 200aa// 100%// AAB47496

BRHIP2005932

BRHIP2006800

BRHIP2007616// plexin 2// 7.5E-137// 423aa// 59%// BAA13189

BRHIP2007741

30 BRHIP2009340

BRHIP2009414// Bax inhibitor-1 (BI-1) (Testis enhanced gene transcript).// 3.00E-97// 177aa// 77%// P55061

BRHIP2009474

BRHIP2013699

35 BRHIP2014228



BRHIP2021615// Homo sapiens CUG-BP and ETR-3 like factor 4 (CELF4) mRNA,  
complete cds.// 9.60E-115// 349aa// 65%// AF329265  
BRHIP2022221  
BRHIP2024146  
5 BRHIP2024165// Synthase [Homo sapiens]// 5.00E-44// 83aa// 94%// NM\_003896  
BRHIP2026061  
BRHIP2026288// Protein bem46.// 2.00E-47// 110aa// 41%// P54069  
BRHIP2029176  
BRHIP2029393// COBW-like protein [Homo sapiens]// 3.00E-89// 158aa// 98%//  
10 NM\_018491  
BRHIP3000339// MYELIN BASIC PROTEIN (MBP).// 8.5E-26// 64aa// 90%// P02686  
BRHIP3000526  
BRHIP3001283  
BRHIP3006683  
15 BRHIP3007483  
BRHIP3007586  
BRHIP3008183  
BRHIP3008313// testis specific ankyrin-like protein 1 [Homo sapiens]// 1.00E-  
120// 210aa// 92%// NM\_016552  
20 BRHIP3008344  
BRHIP3008405// Dynamin 2 (EC 3.6.1.50) (Dynamin UDNM).// 1.00E-56// 108aa//  
90%// P39054  
BRHIP3008565  
BRHIP3008598  
25 BRHIP3008997  
BRHIP3009099  
BRHIP3009448// 2-19 protein precursor.// 1.00E-102// 179aa// 99%// P98173  
BRHIP3011241  
BRHIP3013765  
30 BRHIP3013897  
BRHIP3015751  
BRHIP3016213  
BRHIP3018797  
BRHIP3020182  
35 BRHIP3024118// Monocarboxylate transporter 4 (MCT 4) (MCT 3).// 1.00E-36//  
108aa// 30%// 035910

- BRHIP3024533  
BRHIP3024725  
BRHIP3025161// Putative Rho/Rac guanine nucleotide exchange factor (Rho/Rac GEF) (Faciogenital dysplasia protein homolog).// 2.00E-75// 175aa// 30%//
- 5 P52734  
BRHIP3025702  
BRHIP3026097  
BRHIP3027137// 10-formyltetrahydrofolate dehydrogenase (EC 1.5.1.6) (10-FTHFDH).// 1.00E-119// 208aa// 93%// 075891
- 10 BRHIP3027854// Homo sapiens ectonucleotide pyrophosphatase/phosphodiesterase 2 (autotaxin) (ENPP2)// 1.00E-130// 222aa// 94%// NM\_006209  
BRSSN2000684// CDC14 homolog B, isoform 3 [Homo sapiens]// 3.00E-12// 52aa// 30%// NM\_033332  
BRSSN2003086
- 15 BRSSN2004496// TASP for testis-specific adriamycin sensitivity protein [Homo sapiens]// 5.00E-45// 101aa// 39%// NM\_018697  
BRSSN2004719// SHC transforming protein.// 4.00E-39// 89aa// 53%// P29353  
BRSSN2006892  
BRSSN2008549// oxysterol binding protein 2 [Mus musculus]// 1.00E-149//
- 20 252aa// 75%// NM\_024289  
BRSSN2008797  
BRSSN2011262  
BRSSN2011738  
BRSSN2013874// TEMO [Rattus norvegicus]// 2.00E-53// 99aa// 98%// NM\_023986
- 25 BRSSN2014299// TPA inducible gene-1; TPA inducible protein [Homo sapiens]// 2.00E-47// 93aa// 86%// NM\_015889  
BRSSN2014424// transporter-like protein [Homo sapiens]// 0// 413aa// 92%// NM\_022109  
BRSSN2014556
- 30 BRSSN2018581  
BRSSN2018925  
BRSTN2000872// Protein disulfide isomerase A2 precursor (EC 5.3.4.1) (PDip).// 0// 341aa// 92%// Q130°7  
BRSTN2001067
- 35 BRSTN2001613// HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEINS C1/C2 (HNRNP C1 AND HNRNP C2).// 2.8E-34// 214aa// 43%// P07910

BRSTN2002400  
BRSTN2003835  
BRSTN2004863// *Drosophila melanogaster* polypeptide N-acetylgalactosaminyltransferase mRNA, complete cds.// 5.60E-126// 526aa//  
5 47%// AF158747  
BRSTN2004987// *Homo sapiens* mRNA for mitochondrial tryptophanyl-tRNA synthetase (WARS2 gene).// 1.20E-162// 360aa// 86%// AJ242739  
BRSTN2005721  
BRSTN2006865  
10 BRSTN2007000  
BRSTN2007284  
BRSTN2008052  
BRSTN2008283  
BRSTN2008418// Breakpoint cluster region protein (EC 2.7.1.-).// 7.00E-33//  
15 70aa// 75%// P11274  
BRSTN2008457  
BRSTN2009899  
BRSTN2010363  
BRSTN2010500  
20 BRSTN2010750  
BRSTN2012320  
BRSTN2012380  
BRSTN2013741// Ras-related protein M-Ras (Ras-related protein R-Ras3).//  
1.00E-105// 189aa// 90%// 014807  
25 BRSTN2015015  
BRSTN2016470  
BRSTN2016678  
BRSTN2017084  
BRSTN2017110  
30 BRSTN2017237  
BRSTN2017771// *Homo sapiens* putative BTK-binding protein mRNA, complete cds.// 1.0E-41// 90aa// 99%// AF235049  
BRSTN2018083  
BRSTN2019129  
35 BRTHA1000311  
BRTHA2000855

BRTHA2001462  
 BRTHA2002115  
 BRTHA2002281// Rho guanine nucleotide exchange factor 10 [Homo sapiens].//  
 5.0E-26// 123aa// 39%// NP\_055444.1  
 5 BRTHA2002376  
 BRTHA2002442  
 BRTHA2002493  
 BRTHA2002608// aldehyde dehydrogenase 1A3// 2.00E-19// 46aa// 88%// NP\_000684  
 BRTHA2002808// GAMMA-INTERFERON-INDUCIBLE PROTEIN IP-30 PRECURSOR.// 7.8E-  
 10 65// 141aa// 90%// P13284  
 BRTHA2003030  
 BRTHA2003110// Protein Clorf8 precursor (Liver membrane-bound protein)  
 (HSPC001).// 1.00E-98// 178aa// 92%// Q9BXS4  
 BRTHA2003116  
 15 BRTHA2003461  
 BRTHA2004821  
 BRTHA2004978  
 BRTHA2005579// Xenopus laevis mRNA for Kielin, complete cds.// 1.3E-190//  
 659aa// 47%// AB026192  
 20 BRTHA2005956  
 BRTHA2006075  
 BRTHA2006146  
 BRTHA2006194  
 BRTHA2007122// ANKYRIN 2 (BRAIN ANKYRIN) (ANKYRIN B) (ANKYRIN,  
 25 NONERYTHROID).// 6.1E-18// 203aa// 32%// Q01484  
 BRTHA2007422  
 BRTHA2007603// H.sapiens mRNA for BCL7B protein.// 1.8E-56// 116aa// 98%//  
 X89985  
 BRTHA2008316  
 30 BRTHA2008335  
 BRTHA2008527// LUTROPIN-CHORIOGONADOTROPIC HORMONE RECEPTOR PRECURSOR (LH/CG-  
 R) (LSH-R) (LUTEINIZING HORMONE RECEPTOR).// 7.5E-66// 189aa// 73%// P22888  
 BRTHA2008535  
 BRTHA2008955  
 35 BRTHA2009311// EOSINOPHIL LYSOPHOSPHOLIPASE// 1.0E-30// 64aa// 91%// P97400  
 BRTHA2009846

BRTHA2009972  
BRTHA2010073  
BRTHA2010608  
BRTHA2010884  
5 BRTHA2010907  
BRTHA2011194  
BRTHA2011351  
BRTHA2011500  
BRTHA2011641  
10 BRTHA2012392// Homo sapiens HCDI (HCDI) mRNA, complete cds.// 8.0E-95//  
194aa// 95%// AF226050  
BRTHA2012562  
BRTHA2012980// INTERLEUKIN-13 RECEPTOR ALPHA-1 CHAIN PRECURSOR (IL-13R-ALPHA-  
1) (IL-13RA-1).// 1.5E-44// 91aa// 100%// P78552  
15 BRTHA2013262  
BRTHA2013460  
BRTHA2013707  
BRTHA2014792// ENHANCER OF ZESTE HOMOLOG 1 (ENX-2) (KIAA0388).// 7.1E-21//  
184aa// 35%// Q92800  
20 BRTHA2014828  
BRTHA2015406// Homo sapiens mRNA for putative serine/threonine protein kinase,  
partial.// 1.90E-86// 268aa// 67%// AJ006701  
BRTHA2015478  
BRTHA2015696  
25 BRTHA2015878  
BRTHA2016215  
BRTHA2016496// Vacuolar processing enzyme precursor (EC 3.4.22.-) (VPE).//  
0// 370aa// 79%// P49043  
BRTHA2016543  
30 BRTHA2017353  
BRTHA2017985  
BRTHA2018165  
BRTHA2018344  
BRTHA2018591  
35 BRTHA2018624// Oncorhynchus mykiss stl3 mRNA for rhamnose binding lectin STL3,  
complete cds.// 7.40E-21// 167aa// 34%// AB039024

BRTHA2018707  
 BRTHA2019014  
 BRTHA2019022  
 BRTHA2019048  
 5 BRTHA3000273  
 BRTHA3000297  
 BRTHA3000633// single-pass transmembrane protein [Rattus norvegicus]// 5.00E-48// 220aa// 54%// BAA90767  
 BRTHA3001721// TATA box binding protein (TBP)-associated factor, RNA  
 10 polymerase III, GTF3B subunit 2; TATA box binding protein (TBP)-associated factor, RNA polymerase III, C, 90kD; general transcription factor IIIB, 90kD [Homo sapiens]// 4.00E-71// 135aa// 85%// NM\_001519  
 BRTHA3002401  
 BRTHA3002427// Sodium- and chloride-dependent betaine transporter (Na<sup>+</sup>/Cl<sup>-</sup>-betaine/GABA transporter) (BGT-1).// 0// 553aa// 96%// P48065  
 15 BRTHA3002933// uroplakin 3 [Homo sapiens]// 1.00E-158// 260aa// 99%// XP\_001216  
 BRTHA3003074// putative prostate cancer susceptibility protein; hypothetical protein FLJ10530 [Homo sapiens]// 0// 435aa// 94%// NM\_018127  
 20 BRTHA3003343// DAZ associated protein 1 [Homo sapiens]// 1.00E-95// 223aa// 92%// NP\_061832  
 BRTHA3003449// MYOSIN HEAVY CHAIN, SMOOTH MUSCLE ISOFORM (SMMHC) (FRAGMENT).// 4.70E-215// 400aa// 100%// P35749  
 BRTHA3003474  
 25 BRTHA3003490  
 BRTHA3004475  
 BRTHA3005046  
 BRTHA3006856  
 BRTHA3007113  
 30 BRTHA3007148  
 BRTHA3007319  
 BRTHA3007769  
 BRTHA3008143  
 BRTHA3008310// Mus musculus mRNA for iroquois homeobox protein 6 (Irx6 gene).// 1.20E-176// 444aa// 76%// AJ271055  
 35 BRTHA3008386

- BRTHA3008520// sporulation-induced transcript 4-associated protein;  
hypothetical protein FLJ11058 [Homo sapiens]// 1.00E-164// 287aa// 87%//  
NM\_018312
- 5 BRTHA3008778// Acetyl-coenzyme A synthetase (EC 6.2.1.1) (Acetate—CoA  
ligase) (Acyl- activating enzyme).// 1.00E-168// 286aa// 51%// 068040  
BRTHA3009037// Regulator of G-protein signaling 3 (RGS3) (RGP3).// 0//  
479aa// 92%// P49796
- BRTHA3009090// neuropathy target esterase [Homo sapiens]// 0// 784aa// 60%//  
NM\_006702
- 10 BRTHA3009291  
BRTHA3010366  
BRTHA3013884// Sorting nexin 14 (Fragment).// 0// 359aa// 95%// Q9Y5W7  
BRTHA3015815// Selenide,water dikinase 1 (EC 2.7.9.3) (Selenophosphate  
synthetase 1) (Selenium donor protein 1).// 1.00E-159// 275aa// 99%// P49903
- 15 BRTHA3015910  
BRTHA3016845  
BRTHA3016917// Valyl-tRNA synthetase 2 (EC 6.1.1.9) (Valine—tRNA ligase 2)  
(VALRS 2).// 4.00E-82// 169aa// 43%// P26640  
BRTHA3017047
- 20 BRTHA3017589// junctional adhesion molecule 3 [Homo sapiens]// 1.00E-119//  
213aa// 74%// NM\_031470  
BRTHA3017848// Organic cation/carnitine transporter 2 (Solute carrier family  
22, member 5) (High-affinity sodium-dependent carnitine cotransporter).//  
2.00E-42// 105aa// 35%// 076082
- 25 BRTHA3018514  
BRTHA3018617  
BRTHA3018656  
BRTHA3019105  
CERVX1000042
- 30 CERVX2002006  
COLON1000030  
COLON2000470// Rattus norvegicus nucleolar protein C7C mRNA, complete cds.//  
5.9E-51// 187aa// 49%// AF333986  
COLON2000568// Ig alpha-2 chain C region.// 0// 324aa// 95%// P01877
- 35 COLON2001721// GLUT4 vesicle protein [Mus musculus]// 8.00E-36// 160aa//  
39%// AAD10190

- COLON2002443  
COLON2002520// Myosin heavy chain, nonmuscle type B (Cellular myosin heavy chain, type B) (Nonmuscle myosin heavy chain-B) (NMMHC-B).// 0// 447aa// 70%// Q27991
- 5 COLON2003043  
COLON2004478// protein Tro alpha1 H, myeloma // 3.2E-233// 475aa// 88%// 0501254A  
COLON2005126  
COLON2005772// Homo sapiens candidate taste receptor T2R14 gene, complete
- 10 cds.// 3.9E-54// 112aa// 97%// AF227138  
COLON2006282  
COLON2009499  
CORDB1000140  
CORDB2000061
- 15 CORDB2000541// F-actin capping protein beta subunit (CAPZ beta).// 1.00E-126// 217aa// 99%// P79136  
CTONG1000087  
CTONG1000088  
CTONG1000288
- 20 CTONG1000302  
CTONG1000341// THROMBOMODULIN PRECURSOR (FETOMODULIN) (TM) (CD141 ANTIGEN).// 1.0E-283// 488aa// 99%// P07204  
CTONG1000467// Mus musculus mRNA for Deltex3, complete cds.// 5.00E-54// 203aa// 52%// AB015425
- 25 CTONG1000488  
CTONG1000508  
CTONG1000540  
CTONG2000042// ALPHA-2-MACROGLOBULIN PRECURSOR (ALPHA-2-M).// 2E-132// 841aa// 35%// P01023
- 30 CTONG2001877  
CTONG2004062// ATPase subunit 6 [Homo sapiens].// 3.00E-71// 226aa// 91%// BAA07295  
CTONG2006798// putative serine/threonine protein kinase [Schizosaccharomyces pombe]// 5.80E-69// 581aa// 27%// CAB66438
- 35 CTONG2008233// Bos taurus DnaJ1 protein mRNA, complete cds.// 0// 1376bp// 85%// AF308815



- CTONG2009423// 5-HYDROXYTRYPTAMINE 7 RECEPTOR (5-HT-7) (5-HT-X) (SEROTONIN RECEPTOR) (5HT7).// 2.40E-44// 113aa// 78%// P34969
- CTONG2009531
- CTONG2010803// Regulator of G-protein signaling 3 (RGS3) (RGP3).// 0//
- 5 323aa// 92%// P49796
- CTONG2013178// Homo sapiens serine protease DESC1 (DESC1) mRNA, complete cds.// 2E-90// 421aa// 43%// AF064819
- CTONG2017500// Homo sapiens muscle disease-related protein mRNA, complete cds.// 1.30E-59// 239aa// 47%// AF204674
- 10 CTONG2019248
- CTONG2019652
- CTONG2019704
- CTONG2019788
- CTONG2019833
- 15 CTONG2020026// Drosophila melanogaster BcDNA. GH09358 (BcDNA. GH09358) mRNA, complete cds.// 4.2E-187// 669aa// 45%// AF181639
- CTONG2020127
- CTONG2020522
- CTONG2020638
- 20 CTONG2020806
- CTONG2021132
- CTONG2022153
- CTONG2022601
- CTONG2023021// H.sapiens mRNA for TFG protein.// 2.3E-88// 160aa// 100%//
- 25 Y07968
- CTONG2023512// Homo sapiens PIG-T mRNA for phosphatidylinositol glycan class T, complete cds.// 7.1E-158// 289aa// 100%// AB057724
- CTONG2024206
- CTONG2024749// ALPHA-2-MACROGLOBULIN PRECURSOR (ALPHA-2-M).// 1.1E-174//
- 30 699aa// 46%// P06238
- CTONG2025496// ALPHA-2-MACROGLOBULIN PRECURSOR (ALPHA-2-M).// 1.2E-218//
- 977aa// 45%// P01023
- CTONG2025516// general transcription factor II, i, isoform 3; BTK-associated protein, 135kD; Williams-Beuren syndrome chromosome region 6; Bruton tyrosine
- 35 kinase-associated protein 135; TFII-I protein; SPIN protein [Homo sapiens]//
- 2.00E-28// 57aa// 89%// NM\_033001

CTONG2025900

CTONG2026920

CTONG2027327

CTONG2028124// very long-chain acyl-CoA synthetase homolog 1: VLCS-H1 protein

5 [Homo sapiens]// 5.00E-86// 156aa// 48%// NM\_014031

CTONG2028687

CTONG3000084// PROBABLE GUANINE NUCLEOTIDE REGULATORY PROTEIN TIM (ONCOGENE  
TIM) (P60 TIM) (TRANSFORMING IMMORTALIZED MAMMARY ONCOGENE).// 4.3E-276//

519aa// 100%// Q12774

10 CTONG3000657

CTONG3000686

CTONG3000707

CTONG3000896

CTONG3001123// Mus musculus Pax transcription activation domain interacting  
15 protein PTIP mRNA, complete cds.// 0// 965aa// 84%// AF104261

CTONG3001370// ALPHA-2-MACROGLOBULIN PRECURSOR (ALPHA2M).// 1.5E-267//  
1008aa// 38%// Q61838

CTONG3001420

CTONG3001560

20 CTONG3002020

CTONG3002127// granuphilin [Mus musculus]// 1.00E-104// 204aa// 49%//  
NM\_013757

CTONG3002412// Human DOCK180 protein mRNA, complete cds.// 4.5E-236// 678aa//  
66%// D50857

25 CTONG3002674

CTONG3003179

CTONG3003483

CTONG3003652

CTONG3003654

30 CTONG3003737// PLATELET GLYCOPROTEIN V PRECURSOR (GPV) (CD42D).// 1.80E-73//  
434aa// 37%// 008770

CTONG3003905

CTONG3003972

CTONG3004072// GL002 protein [Homo sapiens]// 3.00E-80// 152aa// 88%//

35 NM\_020193

CTONG3004712

CTONG3005325  
 CTONG3005648  
 CTONG3005713  
 CTONG3005813  
 5 CTONG3006067  
 CTONG3006186// syntaxin binding protein 4 [Mus musculus]// 0// 427aa// 76%//  
 NM\_011505  
 CTONG3006650  
 CTONG3007444  
 10 CTONG3007528  
 CTONG3007586  
 CTONG3007870  
 CTONG3008252  
 CTONG3008258// Homo sapiens GROS1-L protein mRNA, complete cds.// 7.70E-177//  
 15 680aa// 51%// AF097432  
 CTONG3008496  
 CTONG3008566  
 CTONG3008639// Human non-lens beta gamma-crystallin like protein (AIM1) mRNA,  
 partial cds.// 0// 836aa// 99%// U83115  
 20 CTONG3008831// Rattus norvegicus PGC1 mRNA for PPAR gamma coactivator,  
 complete cds.// 2.9E-69// 176aa// 46%// AB025784  
 CTONG3008894// Mus musculus SH3-domain binding protein 5// 3.00E-42// 89aa//  
 40%// NM\_011894  
 CTONG3008951  
 25 CTONG3009028// sno gene product [Drosophila melanogaster]// 1.00E-148//  
 1000aa// 46%// AAF48240  
 CTONG3009227  
 CTONG3009239  
 CTONG3009328  
 30 CTONG3009385// Homo sapiens ARG99 mRNA, complete cds.// 2.4E-77// 153aa//  
 100%// AF319520  
 D30ST2002182// Homo sapiens mRNA for acetylglucosaminyltransferase-like  
 protein.// 6.50E-11// 265aa// 23%// AJ007583  
 D30ST2002648// PUTATIVE G PROTEIN-COUPLED RECEPTOR GPR17 (R12).// 3E-24//  
 35 184aa// 28%// Q13304

- D30ST3000169// Homo sapiens SH3-SAM adaptor protein (HACS1) mRNA, complete cds.// 2.40E-189// 354aa// 99%// AF218085
- DFNES1000107
- DFNES2000146// Mus musculus mRNA for thrombospondin type 1 domain, complete cds.// 4.10E-31// 135aa// 41%// AB016768
- 5 DFNES2001108// Homo sapiens nuclear dual-specificity phosphatase (SBF1) mRNA, partial cds.// 4.5E-41// 134aa// 63%// U93181
- DFNES2005266// ADAM-TS 1 PRECURSOR (EC 3.4.24.-) (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 1) (ADAMTS-1) (ADAM-TS1).//
- 10 4.80E-15// 118aa// 30%// P97857
- DFNES2010502
- DFNES2011239
- DFNES2011499
- ERLTF2000324
- 15 FCBBF1000297// Human protein immuno-reactive with anti-PTH polyclonal antibodies mRNA, partial cds.// 7.5E-186// 359aa// 99%// U28831
- FCBBF2001183
- FCBBF2007510
- FCBBF3001977
- 20 FCBBF3002163// chromosome condensation-related SMC-associated protein 1; chromosome condensation-related SMC-associated protein 1; KIAA0159 gene product [Homo sapiens]// 0// 840aa// 97%// NM\_014865
- FCBBF3003435
- FCBBF3004502
- 25 FCBBF3004847
- FCBBF3006171
- FCBBF3007242
- FCBBF3007540// GUANINE NUCLEOTIDE EXCHANGE FACTOR DBS (DBL'S BIG SISTER)//
- 5.00E-46// 300aa// 38%// 015068
- 30 FCBBF3008944
- FCBBF3009888// Homo sapiens prostate stem cell antigen (PSCA) mRNA, complete cds.// 5.30E-06// 122aa// 32%// AF043498
- FCBBF3012170// Mus musculus rostral cerebellar malformation protein (rcm) mRNA, complete cds.// 1.00E-80// 325aa// 51%// U72634
- 35 FCBBF3012288

FCBBF3013307// Homo sapiens RNA helicase-related protein mRNA, complete  
cds.// 0// 644aa// 99%// AF083255

FCBBF3013846

FCBBF3021576

5 FCBBF3021940// SYNAPSIN I (FRAGMENT).// 5.00E-06// 128aa// 35%// 062732

FCBBF3023443

FCBBF3023895// contains simiarity to tubulin-tyrosine ligase [Caenorhabditis  
elegans].// 1.00E-54// 220aa// 39%// AAF39893

FCBBF3025730

10 FCBBF3027717

FCBBF4000076

FEBRA1000030// T-CELL RECEPTOR BETA CHAIN ANA 11.// 2.7E-11// 131aa// 38%//  
P06333

FEBRA2000253

15 FEBRA2006396

FEBRA2007544// transcription factor [Homo sapiens]// 0// 400aa// 99%//  
AAG33674

FEBRA2007708// DRA PROTEIN (DOWN-REGULATED IN ADENOMA).// 2.60E-72// 511aa//  
34%// P40879

20 FEBRA2007793

FEBRA2007801// Homo sapiens TRIAD3 mRNA, partial cds.// 2.3E-207// 358aa//  
99%// AF228527

FEBRA2008287

FEBRA2008311// GALANIN RECEPTOR TYPE 1 (GAL1-R) (GALR1).// 1E-23// 299aa//  
25 27%// P56479

FEBRA2008360

FEBRA2008468// LYSOSOMAL ACID LIPASE/CHOLESTERYL ESTER HYDROLASE PRECURSOR  
(EC 3.1.1.13) (LAL) (ACID CHOLESTERYL ESTER HYDROLASE) (STEROL ESTERASE)  
(LIPASE A) (CHOLESTERYL ESTERASE).// 1.20E-179// 330aa// 97%// P38571

30 FEBRA2010719

FEBRA2014213

FEBRA2015588

FEBRA2020484

FEBRA2020582

35 FEBRA2020668

FEBRA2020886

- FEBRA2021339  
 FEBRA2021571  
 FEBRA2021908  
 FEBRA2021966  
 5 FEBRA2024136  
 FEBRA2024150  
 FEBRA2024343  
 FEBRA2024744// Homo sapiens Cat Eye Syndrome critical region protein isoform  
 1 mRNA, complete cds.// 1.3E-126// 252aa// 94%// AF273270  
 10 FEBRA2025427  
 FEBRA2026984// TYROSYL-TRNA SYNTHETASE (EC 6.1.1.1) (TYROSYL-TRNA LIGASE)  
 (TYRRS) (FRAGMENT).// 7.80E-271// 528aa// 94%// Q29465  
 FEBRA2027082  
 FEBRA2027297  
 15 FEBRA2027352  
 FEBRA2028366  
 FEBRA2028477  
 FEBRA2028618  
 HCASM2001301// MITOGEN-ACTIVATED PROTEIN KINASE 12 (EC 2.7.1.-)  
 20 (EXTRACELLULAR SIGNAL-REGULATED KINASE 6) (EC 2.7.1.-) (ERK6) (ERK5) (STRESS-  
 ACTIVATED PROTEIN KINASE-3) (MITOGEN-ACTIVATED PROTEIN KINASE P38 GAMMA) (MAP  
 KINASE P38 GAMMA).// 2.2E-52// 104aa// 100%// P53778  
 HCASM2002502  
 HCASM2002918  
 25 HCASM2003212  
 HCASM2003415  
 HCASM2007047  
 HCASM2007737// SEC14-LIKE PROTEIN 1.// 8.30E-09// 162aa// 24%// Q92503  
 HCHON2000028// Homo sapiens 7h3 protein mRNA, partial cds.// 2.1E-94//  
 30 228aa// 82%// AF209931  
 HCHON2000212  
 HCHON2000244  
 HCHON2000418  
 HCHON2000626// X-linked protein STS1769.// 2.00E-47// 89aa// 83%// Q99871  
 35 HCHON2001084// ARABINOSE-PROTON SYMPORTER (ARABINOSE TRANSPORTER).// 3E-66//  
 321aa// 36%// P09830

- HCHON2001217// Homo sapiens cullin CUL4B (CUL4B) mRNA, complete cds.// 0//  
782aa// 99%// AF212995
- HCHON2001548
- HCHON2001577// Human elastin gene, exon 1.// 1.5E-265// 585aa// 88%// M17282
- 5 HCHON2001712// Neutral amino acid transporter B(0) (ATB(0)).// 0// 369aa//  
85%// Q15758
- HCHON2002676// ALPHA-L-IDURONIDASE PRECURSOR (EC 3.2.1.76).// 3.20E-274//  
330aa// 99%// P35475
- HCHON2003532// PHOSPHORYLASE B KINASE BETA REGULATORY CHAIN (PHOSPHORYLASE  
10 KINASE BETA SUBUNIT).// 2.0E-159// 312aa// 95%// Q93100
- HCHON2004007// Potential phospholipid-transporting ATPase IK (EC 3.6.3.13)  
(Fragment).// 1.00E-160// 273aa// 93%// O60423
- HCHON2004531// UV excision repair protein RAD23 homolog B (HHR23B) (XP-C  
repair complementing complex 58 kDa protein) (P58).// 1.00E-142// 270aa//  
15 66%// P54727
- HCHON2004776// transmembrane protein (63kD), endoplasmic reticulum/Golgi  
intermediate compartment [Homo sapiens]// 0// 500aa// 86%// NP\_006816
- HCHON2005921// lipoma HMGIC fusion partner [Homo sapiens]// 1.00E-15// 52aa//  
25%// NM\_005780
- 20 HCHON2006250// Mus musculus SETA binding protein 1 (Sb1) mRNA, complete  
cds.// 3.9E-269// 544aa// 91%// AF246218
- HCHON2006714
- HCHON2007881
- HCHON2008112// Homo sapiens HERC2 (HERC2) mRNA, complete cds.// 1.80E-24//  
25 79aa// 70%// AF071172
- HCHON2008444// 28S ribosomal protein S15, mitochondrial precursor (MPR-S15)  
(DC37).// 5.00E-39// 76aa// 76%// P82914
- HEART1000010// Hepatocyte growth factor-like protein precursor (Macrophage  
stimulatory protein) (MSP) (Macrophage stimulating protein).// 5.00E-18//  
30 40aa// 93%// P26927
- HEART1000074// BANP homolog; putative transcription factor; Btg3 associated  
nuclear protein [Mus musculus]// 0// 420aa// 82%// NM\_016812
- HEART1000088
- HEART1000139// TROPONIN T, CARDIAC MUSCLE ISOFORMS (TNTC).// 1.40E-112//  
35 221aa// 98%// P45379
- HEART2001680// Ig alpha-1 chain C region.// 0// 324aa// 91%// P01876

HEART2001756  
 HEART2006131// 2-hydroxyphytanoyl-CoA lyase [Mus musculus]// 1.00E-138//  
 263aa// 45%// NM\_019975  
 HEART2006909// Hemolysin C.// 3.00E-40// 88aa// 33%// Q54318  
 5 HEART2007031  
 HEART2010391  
 HEART2010492// GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE, MITOCHONDRIAL PRECURSOR  
 (EC 2.3.1.15) (GPAT) (P90).// 3.6E-47// 462aa// 32%// Q61586  
 HEART2010495// MICROTUBULE-ASSOCIATED PROTEIN 4.// 2.00E-159// 579aa// 62%//  
 10 P27816  
 HHDPG1000118// Threonine synthase (EC 4.2.99.2).// 3.00E-70// 178aa// 35%//  
 Q9ZMX5  
 HHDPG2001337  
 HLUNG1000017  
 15 HLUNG2000014// Mus musculus strain BALB/c dectin-2 alpha isoform mRNA,  
 complete cds.// 2.80E-55// 211aa// 50%// AF240357  
 HLUNG2001996  
 HLUNG2002465// Homo sapiens Asef mRNA for APC-stimulated guanine nucleotide  
 exchange factor, complete cds.// 1.30E-183// 557aa// 62%// AB042199  
 20 HLUNG2002958  
 HLUNG2003003  
 HLUNG2003872  
 HLUNG2010464  
 HLUNG2011041// basic proline-rich peptide IB-8a - human (fragments)// 9.7E-  
 25 07// 113aa// 35%// D38355  
 HLUNG2011298// Homo sapiens cytochrome b5 reductase 1 (B5R.1) mRNA, complete  
 cds.// 1.6E-27// 79aa// 78%// AF169481  
 HLUNG2012049  
 HLUNG2012287  
 30 HLUNG2012727  
 HLUNG2013204// phytoene dehydrogenase-like [Arabidopsis thaliana]// 4.0E-53//  
 97aa// 55%// BAB10768  
 HLUNG2013304  
 HLUNG2013622  
 35 HLUNG2013851  
 HLUNG2014262



- HLUNG2014288// Mus musculus RP42 mRNA, complete cds.// 2.4E-40// 189aa//  
43%// AF198092
- HLUNG2014449
- HLUNG2015617
- 5 HLUNG2017350// GAP JUNCTION ALPHA-3 PROTEIN (CONNEXIN 44) (CX44).// 2.60E-  
53// 262aa// 41%// P41987
- HLUNG2017546
- HLUNG2017806
- HLUNG2019058
- 10 HSYRA2004858
- HSYRA2005456
- HSYRA2005496// ENDOGLIN PRECURSOR (CD105 ANTIGEN).// 2.4E-117// 245aa// 92%//  
P17813
- HSYRA2006873
- 15 HSYRA2007667
- HSYRA2008376
- HSYRA2008714// POTENTIAL PHOSPHOLIPID-TRANSPORTING ATPASE ID (EC 3.6.1.-)  
(FRAGMENT).// 6.2E-158// 412aa// 70%// P98198
- HSYRA2009075
- 20 HSYRA2009102// UDP-galactose transporter related [Homo sapiens].// 3.0E-26//  
280aa// 32%// NP\_005818
- IMR322000127// ZINC FINGER PROTEIN 135.// 3.30E-130// 426aa// 50%// P52742
- IMR322000917// ZINC FINGER PROTEIN 29 (ZFP-29).// 1.50E-34// 197aa// 40%//  
Q07230
- 25 IMR322001380// Homo sapiens leucine-rich repeats containing F-box protein  
FBL3 mRNA, complete cds.// 7.00E-21// 216aa// 32%// AF186273
- IMR322002035
- IMR322002110
- IMR322003675
- 30 IMR322006222
- IMR322006495// Homo sapiens mRNA for kinetochore protein CENP-H, complete  
cds.// 3.1E-61// 183aa// 73%// AB035124
- IMR322006886// Homo sapiens hepatocellular carcinoma-associated antigen 127  
(HCA127) mRNA, complete cds.// 2.5E-107// 207aa// 99%// AF270491
- 35 IMR322007225
- IMR322016146

IMR322018117  
 KIDNE1000064// Mus musculus mRNA for RST, complete cds.// 6.70E-219// 552aa//  
 73%// AB005451  
 KIDNE2000665  
 5 KIDNE2000722  
 KIDNE2000832  
 KIDNE2000846// Mus musculus orphan transporter isoform A12 (Xtrp2) mRNA,  
 alternatively spliced, complete cds.// 1.2E-54// 203aa// 50%// AF075262  
 KIDNE2001361// Mus musculus catp mRNA for cation-transporting atpase,  
 10 complete cds.// 4.1E-123// 273aa// 91%// AB035381  
 KIDNE2001847// H.sapiens graf gene.// 4.10E-98// 300aa// 55%// Y10388  
 KIDNE2002252// Drosophila melanogaster BcDNA. GH09358 (BcDNA. GH09358) mRNA,  
 complete cds.// 6.30E-145// 763aa// 42%// AF181639  
 KIDNE2002991  
 15 KIDNE2003837  
 KIDNE2005543  
 KIDNE2006580// CYTOCHROME P450 4C1 (EC 1.14.14.1) (CYP1VC1).// 1.10E-119//  
 496aa// 49%// P29981  
 KIDNE2010264  
 20 KIDNE2011314  
 KIDNE2011532// similar to melanoma-associated chondroitin sulfate  
 proteoglycan 4// 7.00E-30// 54aa// 60%// XP\_000655  
 KIDNE2011635// Rabbit mRNA for sodium-glucose cotransporter, complete cds.//  
 2.1e-313// 670aa// 80%// D16226  
 25 KIDNE2012945// PROCOLLAGEN C-PROTEINASE ENHANCER PROTEIN PRECURSOR (PCPE)  
 (TYPE I PROCOLLAGEN COOH-TERMINAL PROTEINASE ENHANCER) (TYPE 1 PROCOLLAGEN C-  
 PROTEINASE ENHANCER PROTEIN).// 2.00E-14// 113aa// 41%// Q15113  
 KIDNE2013095  
 LIVER2007415  
 30 LYMPB1000141  
 LYMPB2000083// HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, ALPHA CHAIN F  
 PRECURSOR (HLA F ANTIGEN) (LEUKOCYTE ANTIGEN F).// 4.80E-131// 158aa// 93%//  
 P33617  
 MESAN2001979  
 35 MESAN2006563  
 MESAN2012054

MESAN2014295  
 MESAN2015515  
 MESAN2018576  
 MESTC1000042  
 5 MESTC2000153  
 NB9N41000340  
 NCRRP1000129  
 NESOP2000744  
 NESOP2001433// ALC1\_HUMAN Ig alpha-1 chain C region// 0// 353aa// 100%//  
 10 P01876  
 NESOP2001656  
 NESOP2001694// H.sapiens graf gene.// 7.4E-53// 162aa// 66%// Y10388  
 NESOP2001752  
 NESOP2002738  
 15 NHNPC2000606  
 NHNPC2000877  
 NHNPC2001223  
 NHNPC2001816  
 NHNPC2002565  
 20 NHNPC2002749  
 NOVAR2000136// Calsequestrin, skeletal muscle isoform precursor (Aspartactin)  
 (Laminin-binding protein).// 1.00E-142// 235aa// 66%// P07221  
 NOVAR2000710  
 NOVAR2000962  
 25 NOVAR2001108// Human (hybridoma H210) anti-hepatitis A IgG variable region,  
 constant region, complementarity-determining regions mRNA, complete cds.//  
 3.0E-230// 482aa// 88%// M87789  
 NOVAR2001783  
 NT2NE2003252// Human putative serine/threonine protein kinase PRK (prk) mRNA,  
 30 complete cds.// 3.00E-44// 234aa// 38%// U56998  
 NT2NE2005890  
 NT2NE2006531// ZINC FINGER PROTEIN 184 (FRAGMENT).// 4.10E-113// 437aa//  
 47%// Q99676  
 NT2NE2006909// Methionine aminopeptidase 2 (EC 3.4.11.18) (MetAP 2)  
 35 (Peptidase M 2) (Initiation factor 2 associated 67 kDa glycoprotein) (P67).//  
 1.00E-147// 258aa// 80%// P50579

NT2NE2008060  
 NT2RI2003993  
 NT2RI2004618// Cytosolic acyl coenzyme A thioester hydrolase (EC 3.1.2.2)  
 (Long chain acyl-CoA thioester hydrolase) (CTE-II) (Brain acyl-CoA hydrolase)  
 5 (BACH).// 1.00E-126// 222aa// 88%// 000154  
 NT2RI2005166// VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.// 7.70E-14//  
 300aa// 26%// Q00808  
 NT2RI2006686// E1A-ASSOCIATED PROTEIN P300.// 1.30E-18// 421aa// 26%// Q09472  
 NT2RI2008724  
 10 NT2RI2009855  
 NT2RI2011422// Homo sapiens partial mRNA for transport-secretion protein 2.1  
 (TTS-2.1 gene).// 6.4E-70// 428aa// 40%// AJ278475  
 NT2RI2011683  
 NT2RI2012659  
 15 NT2RI2012990// 76.5 KDA PROTEIN C21ORF13.// 1.8E-73// 149aa// 100%// 095447  
 NT2RI2013357  
 NT2RI2014247  
 NT2RI2014551  
 NT2RI2014733  
 20 NT2RI2016128  
 NT2RI2018311  
 NT2RI2018883  
 NT2RI2019751  
 NT2RI2023303  
 25 NT2RI2025909// carnitine/acylcarnitine translocase// 3.0E-32// 260aa// 37%//  
 NP\_000378  
 NT2RI2025957// LU1 protein [Homo sapiens]// 0// 630aa// 99%// AAF74512  
 NT2RI2027081  
 NT2RI2027396  
 30 NT2RI3000622  
 NT2RI3001263  
 NT2RI3001515// ALEX1 protein [Homo sapiens]// 2.0E-25// 220aa// 29%//  
 NP\_057692  
 NT2RI3002303  
 35 NT2RI3002842  
 NT2RI3002892

NT2RI3003031  
 NT2RI3003095  
 NT2RI3003162  
 NT2RI3003382  
 5 NT2RI3003409  
 NT2RI3004381  
 NT2RI3004510  
 NT2RI3005202  
 NT2RI3005403  
 10 NT2RI3005724  
 NT2RI3006132  
 NT2RI3006171// CARCINOEMBRYONIC ANTIGEN PRECURSOR (CEA) (MECONIUM ANTIGEN  
 100) (CD66E ANTIGEN).// 1.3E-54// 294aa// 39%// P06731  
 NT2RI3006284// Homo sapiens chorea-acanthocytosis (CHAC) mRNA, complete  
 15 cds.// 1.2E-144// 538aa// 51%// AF337532  
 NT2RI3006340// Myomesin 1 (Skelemin).// 0// 1390aa// 81%// Q62234  
 NT2RI3006376  
 NT2RI3006673// LAR protein precursor (Leukocyte antigen related) (EC  
 3.1.3.48).// 0// 1151aa// 90%// P10586  
 20 NT2RI3006796  
 NT2RI3007065  
 NT2RI3007158  
 NT2RI3007291  
 NT2RI3007543  
 25 NT2RI3007757// breast cancer nuclear receptor-binding auxiliary protein //  
 1.00E-172// 295aa// 94%// AAD21311  
 NT2RI3007978// CTP synthase II: CTP synthetase type 2 [Homo sapiens]// 0//  
 536aa// 91%// NM\_019857  
 NT2RI3008055  
 30 NT2RI3008162  
 NT2RI3008652// Homo sapiens mRNA for CDEP, complete cds.// 6.10E-113//  
 443aa// 52%// AB008430  
 NT2RI3008697// erythroblast macrophage protein [Mus musculus]// 2.00E-14//  
 70aa// 25%// NM\_021500  
 35 NT2RI3008974// probable transposase - human transposon MER37// 1.20E-52//  
 165aa// 69%// S72481

- NT2RI3009158// Iroquois-class homeodomain protein IRX-3.// 4.00E-16// 52aa//  
36%// P81067
- NT2RP7000359// PROTEIN-TYROSINE PHOSPHATASE D1 (EC 3.1.3.48).// 6.80E-25//  
319aa// 28%// Q16825
- 5 NT2RP7000466// Cegp1 protein// 0// 482aa// 89%// NP\_064436  
NT2RP7004027// BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (EC 3.4.24.-) (BMP-  
1).// 9.50E-33// 301aa// 30%// P98063  
NT2RP7004123
- NT2RP7005118// RAS GTPASE-ACTIVATING-LIKE PROTEIN IQGAP1 (P195) (KIAA0051).//  
10 0// 1034aa// 58%// P46940  
NT2RP7005529// PROBABLE GUANINE NUCLEOTIDE REGULATORY PROTEIN TIM (ONCOGENE  
TIM) (P60 TIM) (TRANSFORMING IMMORTALIZED MAMMARY ONCOGENE).// 5.40E-56//  
364aa// 37%// Q12774  
NT2RP7005846
- 15 NT2RP7009030  
NT2RP7009147// CHE-2 protein [Caenorhabditis elegans]// 1.00E-177// 740aa//  
41%// CAB38019  
NT2RP7009867  
NT2RP7010128
- 20 NT2RP7010599// Homo sapiens endothelial lipase mRNA, complete cds.// 5.60E-  
174// 321aa// 98%// AF118767  
NT2RP7011570  
NT2RP7013795// VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.// 4.90E-11//  
129aa// 34%// Q00808
- 25 NT2RP7014005// CTP synthase II; CTP synthetase type 2 [Homo sapiens]// 0//  
536aa// 91%// NM\_019857  
NT2RP7015512  
NT2RP7017365  
NT2RP7017474
- 30 NT2RP7017546  
NT2RP8000137  
NT2RP8000296// similar to Kelch proteins// 0// 600aa// 99%// AAF03529  
NT2RP8000483// Rattus norvegicus mRNA for Nadrin E2, complete cds.// 2.00E-  
208// 548aa// 75%// AB060557

- NTONG2000413// MATRIX METALLOPROTEINASE-16 PRECURSOR (EC 3.4.24.-) (MMP-16) (MEMBRANE-TYPE MATRIX METALLOPROTEINASE 3) (MT-MMP 3) (MTMMP3) (MMP-X2).// 5.60E-62// 290aa// 37%// P51512
- NTONG2003852
- 5 NTONG2005277// ANKYRIN 1 (ERYTHROCYTE ANKYRIN).// 8.20E-31// 363aa// 31%// Q02357
- NTONG2005969
- NTONG2006354
- NTONG2007249
- 10 NTONG2007517// RING CANAL PROTEIN (KELCH PROTEIN).// 9.10E-32// 295aa// 28%// Q04652
- NTONG2008088
- NTONG2008672// final exon in repeat region: similar to long tandem repeat region of sialidase (SP:TCNA\_TRYCR, P23253) and neurofilament H protein //
- 15 1.9E-15// 559aa// 25%// AAC48204
- OCBBF1000254
- OCBBF2001794
- OCBBF2002124// p40 [Homo sapiens]// 3.00E-63// 103aa// 88%// AAC51270
- OCBBF2003819
- 20 OCBBF2004826// T-cell lymphoma invasion and metastasis 2 [Homo sapiens]// 0// 580aa// 99%// NP\_036586
- OCBBF2004883
- OCBBF2005428
- OCBBF2006005// Bos taurus phosphatidic acid-preferring phospholipase A1 mRNA, complete cds.// 0// 885aa// 90%// AF045022
- 25 OCBBF2006058// Homo sapiens acyl-Coenzyme A dehydrogenase-8 precursor, mRNA, complete cds.// 5.40E-57// 109aa// 100%// AF126245
- OCBBF2006151// Mus musculus protein tyrosine phosphatase-like protein PTP1b (Ptp1b) mRNA, complete cds.// 3.40E-126// 258aa// 93%// AF169286
- 30 OCBBF2006567
- OCBBF2006764// seizure related gene 6 [Mus musculus]// 0// 780aa// 89%// NP\_067261
- OCBBF2007028// Homo sapiens mRNA for NESCA, complete cds.// 1.50E-169// 176aa// 98%// AB026894
- 35 OCBBF2007068// ankyrin 1 [Bos taurus].// 1.00E-68// 800aa// 32%// AAF61702
- OCBBF2007114

OCBBF2007428  
 OCBBF2007478  
 OCBBF2007610// PSD-95/SAP90-associated protein-4 [Rattus norvegicus].//  
 1.00E-137// 226aa// 90%// AAB48590  
 5 OCBBF2008770  
 OCBBF2009788  
 OCBBF2009926  
 OCBBF2010140  
 OCBBF2010416  
 10 OCBBF2017516  
 OCBBF2019327  
 OCBBF2019823// lactate dehydrogenase A -like [Homo sapiens]// 1.00E-164//  
 273aa// 82%// NM\_033195  
 OCBBF2020343  
 15 OCBBF2020453  
 OCBBF2020639  
 OCBBF2020741  
 OCBBF2020801// Ataxin 7 (Spinocerebellar ataxia type 7 protein).// 5.00E-67//  
 116aa// 100%// 015265  
 20 OCBBF2020838// FORKHEAD BOX PROTEIN D4 (FORKHEAD-RELATED PROTEIN FKHL9)  
 (FORKHEAD-RELATED TRANSCRIPTION FACTOR 5) (FREAC-5) (TRANSCRIPTION FACTOR  
 FKH- 2).// 1.70E-114// 371aa// 63%// Q60688  
 OCBBF2021020// Homo sapiens mRNA for vascular Rab-GAP/TBC-containing protein,  
 complete cds.// 1.8E-24// 107aa// 47%// AB024057  
 25 OCBBF2021286  
 OCBBF2021323// Mus musculus GTRGE022 (Gtrgeo22) mRNA, complete cds.// 7.80E-  
 49// 115aa// 88%// AF303106  
 OCBBF2021788// Homo sapiens mRNA for B-cell CLL/lymphoma 9 (BCL9 gene).//  
 1.30E-92// 600aa// 42%// Y13620  
 30 OCBBF2022351// TIPD PROTEIN.// 1.1E-54// 263aa// 40%// 015736  
 OCBBF2022574  
 OCBBF2023162  
 OCBBF2023643  
 OCBBF2024719  
 35 OCBBF2024781  
 OCBBF2024850



OCBBF2025028  
OCBBF2025458  
OCBBF2025527// GLYCEROL-3-PHOSPHATE DEHYDROGENASE [NAD+], CYTOPLASMIC (EC  
1.1.1.8) (GPD-C) (GPDH-C).// 8.60E-49// 116aa// 78%// P13707  
5 OCBBF2025730  
OCBBF2026645  
OCBBF2027423  
OCBBF2027478  
OCBBF2028173// JM11 protein [Homo sapiens]// 1.00E-131// 304aa// 97%//  
10 AAF05832  
OCBBF2028935  
OCBBF2029901  
OCBBF2030354// Mus musculus pantothenate kinase 1 beta (panK1beta) mRNA,  
complete cds.// 9.50E-195// 372aa// 96%// AF200357  
15 OCBBF2030517  
OCBBF2030574  
OCBBF2030708  
OCBBF2031167// Homo sapiens mRNA for MDC2 alpha, MDC2 beta, complete cds.//  
0// 813aa// 99%// AB009671  
20 OCBBF2031366  
OCBBF2032590// H.sapiens mRNA for melanoma-associated chondroitin sulfate  
proteoglycan (MCSP).// 1.80E-11// 151aa// 39%// X96753  
OCBBF2032599  
OCBBF2032611  
25 OCBBF2032671  
OCBBF2033869// PROCOLLAGEN C-PROTEINASE ENHANCER PROTEIN PRECURSOR (PCPE)  
(TYPE I PROCOLLAGEN COOH-TERMINAL PROTEINASE ENHANCER) (TYPE 1 PROCOLLAGEN C-  
PROTEINASE ENHANCER PROTEIN).// 6.6E-21// 151aa// 38%// Q15113  
OCBBF2035110  
30 OCBBF2035214  
OCBBF2035564  
OCBBF2035885  
OCBBF2035916  
OCBBF2036476  
35 OCBBF2036743// ZINC FINGER PROTEIN 133.// 9.00E-157// 639aa// 48%// P52736

- OCBBF2037068// BCL2/adenovirus E1B 19-kDa protein-interacting protein 2.//  
3.00E-74// 122aa// 66%// 054940  
OCBBF2037340// Sacsin.// 0// 356aa// 100%// Q9NZJ4  
OCBBF2037398
- 5 OCBBF2037547// T-cell lymphoma invasion and metastasis 2 [Homo sapiens]// 0//  
1024aa// 92%// NM\_012454  
OCBBF2037598// axonal-associated cell adhesion molecule [Mus musculus]// 0//  
366aa// 89%// NP\_031544  
OCBBF2037638
- 10 OCBBF2038317// VPS10 domain receptor protein SORCS [Mus musculus]// 0//  
986aa// 91%// NM\_021377  
OCBBF3000296  
OCBBF3000483  
OCBBF3002553
- 15 OCBBF3002600  
OCBBF3003320// Potential phospholipid-transporting ATPase 1S (EC 3.6.3.13)  
(Fragment).// 1.00E-110// 179aa// 62%// P98196  
OCBBF3003592// Dynein beta chain, flagellar outer arm.// 2.00E-54// 222aa//  
21%// Q39565
- 20 OCBBF3004314// Fas apoptotic inhibitory molecule [Mus musculus]// 8.00E-67//  
117aa// 90%// NM\_011810  
OCBBF3006802  
OCBBF3007516  
OCBBF3008230
- 25 OCBBF3009279  
PEBLM2000170// Sprouty homolog 3 (Spry-3).// 1.00E-31// 64aa// 100%// 043610  
PEBLM2000338  
PEBLM2001465// diphthamide biosynthesis; Dph5p [Saccharomyces cerevisiae]//  
9.00E-65// 160aa// 57%// NP\_013273
- 30 PEBLM2001488  
PEBLM2002594// ATP-binding cassette, sub-family A member 8 [Homo sapiens]//  
4.50E-156// 469aa// 64%// XP\_016390  
PEBLM2002749  
PEBLM2002887// ZINC FINGER PROTEIN 195.// 1.50E-08// 62aa// 58%// 014628
- 35 PEBLM2004497  
PEBLM2004666

PEBLM2005183// 5'-3' exonuclease // 0// 804aa// 92%// CAA62819  
 PEBLM2005697  
 PEBLM2006113  
 PEBLM2007112  
 5 PEBLM2007140  
 PEBLM2007834  
 PERIC1000147  
 PERIC2000889// Rattus norvegicus dynamin-like protein variant 4 mRNA,  
 alternatively spliced, partial cds.// 3.1E-22// 51aa// 98%// AF107048  
 10 PERIC2000914  
 PERIC2001227  
 PERIC2001228  
 PERIC2002766  
 PERIC2003090  
 15 PERIC2003452  
 PERIC2003699  
 PERIC2003720// kinectin 1: CG-1 antigen [Homo sapiens].// 2.00E-92// 270aa//  
 90%// NP\_004977  
 PERIC2003834  
 20 PERIC2004028// Mus musculus erythroblast macrophage protein EMP mRNA,  
 complete cds.// 3.80E-33// 65aa// 100%// AF263247  
 PERIC2004259  
 PERIC2004379  
 PERIC2004429  
 25 PERIC2004909  
 PERIC2005347// alpha 1C adrenergic receptor isoform 2// 3.30E-22// 74aa//  
 70%// BAA06901  
 PERIC2005370  
 PERIC2006035  
 30 PERIC2007914// Ubiquitously transcribed TPR gene on Y chromosome [Homo  
 sapiens]// 1.0E-22// 84aa// 67%// NP\_009056  
 PERIC2008385// sarcosine dehydrogenase; dimethylglycine dehydrogenase-like 1  
 [Homo sapiens]// 4.00E-17// 47aa// 51%// NM\_007101  
 PERIC2009086// Homo sapiens melanoma-associated antigen MG50 mRNA, partial  
 35 cds.// 5.00E-189// 508aa// 66%// AF200348  
 PLACE5000001

- PLACE5000171// E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1) (ELAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 2) (LECAM2) (CD62E).// 1.50E-28// 242aa// 30%// P98110  
PLACE5000260
- 5 PLACE5000282// elastin [Homo sapiens]// 8.00E-08// 420aa// 97%// NP\_000492  
PLACE6001185  
PLACE6009006  
PLACE6012574  
PLACE6019385// MITOGEN-ACTIVATED PROTEIN KINASE KINASE KINASE 5 (EC 2.7.1.-)  
10 (MAPK/ERK KINASE KINASE 5) (MEK KINASE 5) (MEKK 5) (APOPTOSIS SIGNAL-REGULATING KINASE 1) (ASK-1).// 2E-57// 92aa// 63%// Q99683  
PLACE6019932// Ictalurus punctatus NCC receptor protein 1 (NCCRP-1) mRNA, complete cds.// 1.2E-34// 124aa// 50%// AF208795  
PLACE6020031// ANKYRIN HOMOLOG PRECURSOR.// 2.70E-06// 156aa// 35%// Q06527  
15 PLACE7000514// Mus musculus mRNA for ER protein 58 (EP58 gene).// 3.80E-111// 366aa// 55%// AJ404004  
PLACE7001022  
PLACE7001936  
PLACE7002641// Ring assembly protein 3.// 2.00E-13// 79aa// 26%// 074994  
20 PLACE7006051// cytoplasmic dynein heavy chain 2 [Rattus norvegicus]// 0// 987aa// 90%// NM\_023024  
PLACE7008431// Phosphatidylinositol-4-phosphate 5-kinase type II alpha (EC 2.7.1.68) (PIP5KII-alpha) (1-phosphatidylinositol-4-phosphate kinase) (PtdIns(4)P-5-kinase B isoform) (Diphosphoinositide kinase).// 1.00E-109//  
25 200aa// 56%// 070172  
PLACE7008623  
PROST1000184// VASOACTIVE INTESTINAL POLYPEPTIDE RECEPTOR 1 PRECURSOR (VIP-R-1) (PITUITARY ADENYLATE CYCLASE ACTIVATING POLYPEPTIDE TYPE II RECEPTOR) (PACAP TYPE II RECEPTOR) (PACAP-R-2).// 7.0E-63// 125aa// 98%// P32241  
30 PROST1000528  
PROST1000559// predicted osteoblast protein [Homo sapiens]// 6.00E-33// 227aa// 38%// NP\_055703  
PROST2003428// Protein pM5 precursor.// 9.00E-47// 91aa// 89%// Q15155  
PROST2008993// Mus musculus Pax transcription activation domain interacting  
35 protein PTIP mRNA, complete cds.// 1.10E-211// 542aa// 77%// AF104261  
PROST2015243

- PROST2016462// N-chimaerin (NC) (N-chimerin) (Alpha chimerin) (A-chimaerin).// 6.00E-26// 65aa// 34%// P30337
- PROST2017367// PROTEIN-GLUTAMINE GLUTAMYLTRANSFERASE 4 (EC 2.3.2.13) (PROSTATE TRANSGLUTAMINASE) (PROSTATE TRANSGLUTAMINASE) (TGP).// 1.30E-52//
5. 102aa// 99%// P49221
- PROST2017413
- PROST2017700
- PROST2018030
- PROST2018090// SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR.// 9.50E-244//
- 10 414aa// 99%// P78539
- PROST2018511// Growth factor receptor-bound protein 7 (GRB7 adapter protein) (Epidermal growth factor receptor GRB-7) (B47).// 0// 495aa// 99%// Q14451
- PROST2018902
- PROST2018922
- 15 PROST2019296
- PROST2019781
- PUAEN2002489// Homo sapiens putative seven pass transmembrane protein (TM7SF1) mRNA, complete cds.// 1.0E-48// 189aa// 53%// AF027826
- PUAEN2002616
- 20 PUAEN2003079// nasopharyngeal carcinoma susceptibility protein [Homo sapiens]// 3.00E-36// 75aa// 96%// NP\_037407
- PUAEN2005588
- PUAEN2005930
- PUAEN2006328// vascular Rab-GAP/TBC-containing [Homo sapiens]// 8.0E-99//
- 25 360aa// 53%// NP\_008994
- PUAEN2006701
- PUAEN2007044// TRNA PSEUDOURIDINE SYNTHASE B (EC 4.2.1.70) (TRNA PSEUDOURIDINE 55 SYNTHASE) (PSI55 SYNTHASE) (PSEUDOURIDYLATE SYNTHASE) (URACIL HYDROLYASE).// 7.90E-15// 129aa// 34%// P45142
- 30 PUAEN2007785
- PUAEN2009174
- PUAEN2009655// Bos taurus phosphatidic acid-preferring phospholipase A1 mRNA, complete cds.// 0// 565aa// 96%// AF045022
- PUAEN2009795// Endothelial cell multimerin precursor.// 1.00E-161// 296aa//
- 35 78%// Q13201

- PUAEN2009852// serine/threonine protein kinase Kp78 splice variant CTAK75a // 3.00E-33// 86aa// 36%// AAD48007  
 RECTM2000433// ZG-16p [Rattus norvegicus] // 1.60E-64// 148aa// 85%// CAA83059
- 5 RECTM2001347// sphingosine kinase type 2 isoform [Homo sapiens]// 4.00E-46// 87aa// 80%// NM\_020126  
 SKMUS2000757  
 SKMUS2003074  
 SKMUS2004047
- 10 SKMUS2006394// Mus musculus ankyrin repeat-containing protein Asb-4 mRNA, partial cds.// 6.40E-54// 405aa// 34%// AF155355  
 SKNMC1000124// putative nuclear protein [Homo sapiens].// 3.00E-12// 398aa// 37%// NP\_057689  
 SKNMC2002402
- 15 SKNMC2004457  
 SKNMC2004643  
 SKNMC2005772  
 SKNMC2006998// PROTEIN PHOSPHATASE INHIBITOR 1 (IPP-1) (I-1).// 9.9E-32// 113aa// 64%// Q13522
- 20 SKNMC2007504// DNA-directed RNA polymerase II largest subunit (EC 2.7.7.6) (RPB1).// 1.00E-16// 76aa// 26%// P08775  
 SKNMC2007961  
 SKNMC2009450  
 SKNSH2000482
- 25 SKNSH2009991  
 SKNSH2010015  
 SMINT1000192// PUTATIVE ATP-DEPENDENT RNA HELICASE KIAA0134.// 4.00E-12// 37aa// 100%// Q14147  
 SMINT2001818
- 30 SMINT2002743  
 SMINT2006641  
 SMINT2007391  
 SMINT2009902  
 SMINT2010076// Ig alpha-1 chain C region.// 0// 319aa// 91%// P01876
- 35 SMINT2010897  
 SMINT2011311

- SMINT2011888// protein Tro alpha1 H, myeloma// 8.9E-215// 481aa// 82%//  
0501254A
- SMINT2015787// immunoglobulin lambda light chain [Homo sapiens]// 1.40E-60//  
164aa// 77%// CAA40954
- 5 SPLEN2001599// Homo sapiens sialic acid binding immunoglobulin-like lectin 8  
long splice variant (Siglec8) gene, complete cds.// 4.00E-71// 294aa// 38%//  
AF287892
- SPLEN2002147// Halocynthia roretzi mRNA for HrPET-3, complete cds.// 1.20E-  
09// 78aa// 41%// AB029335
- 10 SPLEN2002467// Homo sapiens leucine-rich repeats containing F-box protein  
FBL3 mRNA, complete cds.// 1.60E-187// 422aa// 77%// AF186273
- SPLEN2002707
- SPLEN2006122// Homo sapiens RNA-binding region (RNP1, RRM) containing 2  
(RNPC2)// 2.00E-81// 147aa// 84%// NM\_004902
- 15 SPLEN2009548
- SPLEN2010912// putative nucleolar RNA helicase [Homo sapiens]// 0// 339aa//  
90%// NM\_019082
- SPLEN2011422// CALDESMON (CDM).// 5.3E-12// 165aa// 37%// Q05682
- SPLEN2012624// BRCA1-associated RING domain protein 1 (BARD-1).// 6.00E-14//  
20 48aa// 39%// Q9QZH2
- SPLEN2012889// putative Na<sup>+</sup>-dependent inorganic phosphate cotransporter//  
9.00E-19// 70aa// 32%// AAC35230
- SPLEN2014946
- SPLEN2015158
- 25 SPLEN2015267// Homo sapiensIGHG3 gene for immunoglobulin heavy chain gamma 3  
constant region, 4-exon hinge, isolate Lib-A2.// 1.0E-213// 377aa// 100%//  
AJ390247
- SPLEN2015679// Oryctolagus cuniculus sarcolemmal associated protein-3 mRNA,  
complete cds.// 4.90E-30// 266aa// 31%// U21157
- 30 SPLEN2016554
- SPLEN2016863
- SPLEN2017104
- SPLEN2021701// HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-2 ALPHA CHAIN  
PRECURSOR.// 4.40E-128// 173aa// 86%// P01892
- 35 SPLEN2023733
- SPLEN2023791

SPLN2024127  
SPLN2025491  
SPLN2027268  
SPLN2028844  
5 SPLN2028914  
SPLN2029051  
SPLN2029176  
SPLN2029522  
SPLN2029683  
10 SPLN2029727  
SPLN2029912  
SPLN2030335// Mus musculus fatty acid transport protein 3 mRNA, partial  
cds// 9.7E-251// 275aa// 81%// AF072758  
SPLN2030479  
15 SPLN2031125  
SPLN2031424  
SPLN2031547// Triose phosphate/phosphate translocator, non-green plastid  
precursor (CTPT).// 4.00E-20// 76aa// 25%// P52178  
SPLN2031724  
20 SPLN2031780  
SPLN2032154// NDRG1 PROTEIN (DIFFERENTIATION-RELATED GENE 1 PROTEIN) (DRG1)  
(REDUCING AGENTS AND TUNICAMYCIN-RESPONSIVE PROTEIN) (RTP) (NICKEL- SPECIFIC  
INDUCTION PROTEIN CAP43).// 1.0E-22// 80aa// 57%// Q92597  
SPLN2032321  
25 SPLN2032813  
SPLN2033098// tumor necrosis factor receptor superfamily, member 14// 1.7E-  
99// 183aa// 100%// NP\_003811  
SPLN2033153  
SPLN2033539  
30 SPLN2033921  
SPLN2034021  
SPLN2034081  
SPLN2034678  
SPLN2034781  
35 SPLN2036103



SPLEN2036326// CLAUDIN-5 (TRANSMEMBRANE PROTEIN DELETED IN VCFS) (TMDVCF).//  
 2.6E-118// 218aa// 100%// 000501  
 SPLEN2036712  
 SPLEN2036821// MITOCHONDRIAL CARNITINE/ACYLCARNITINE CARRIER PROTEIN  
 5 (CARNITINE/ACYLCARNITINE TRANSLOCASE) (CAC).// 6.5E-10// 104aa// 33%// 043772  
 SPLEN2036932// Homo sapiens calcium and DAG-regulated guanine nucleotide  
 exchange factor I mRNA, complete cds.// 3.9E-63// 124aa// 100%// AF081194  
 SPLEN2037194// NORQ PROTEIN.// 5.5E-11// 127aa// 38%// Q51664  
 SPLEN2037580  
 10 SPLEN2037630  
 SPLEN2037722// lymphocyte antigen 108 [Mus musculus]// 3.00E-63// 137aa//  
 42%// NM\_030710  
 SPLEN2038055  
 SPLEN2038180  
 15 SPLEN2038345  
 SPLEN2038407// basement membrane-induced gene // 2.1E-33// 283aa// 34%//  
 XP\_001646  
 SPLEN2039697  
 SPLEN2039936  
 20 SPLEN2040222  
 SPLEN2041304  
 SPLEN2041310  
 SPLEN2041645  
 SPLEN2041720  
 25 SPLEN2041977  
 SPLEN2042303  
 SPLEN2042598  
 STOMA1000189  
 STOMA2003444  
 30 STOMA2004294// Ig lambda chain V-IV region Bau.// 1.00E-41// 79aa// 73%//  
 P01715  
 STOMA2004925  
 STOMA2008546// CDM PROTEIN (6C6-AG TUMOR-ASSOCIATED ANTIGEN) (DXS1357E).//  
 5.00E-124// 246aa// 100%// P51572  
 35 SYN0V1000374

SYNOV2005216// Homo sapiens laryngeal carcinoma related protein 1 mRNA,  
 complete cds.// 2.5E-36// 70aa// 98%// AF268387  
 SYNOV2005448  
 SYNOV2005817// CYTOKINE RECEPTOR CLASS-III CRF2-4 PRECURSOR.// 7.6E-176//  
 5 314aa// 98%// Q08334  
 SYNOV2006430  
 SYNOV2007965// Homo sapiens mRNA for H-I(3)mbt-like protein, alternative  
 variant a.// 3.1E-118// 429aa// 54%// AJ305226  
 SYNOV2012326// PUTATIVE PROTEIN-TYROSINE PHOSPHATASE TPTE (EC 3.1.3.48).//  
 10 6.7E-24// 112aa// 58%// P56180  
 SYNOV2014400// FIBULIN-1, ISOFORM C PRECURSOR.// 4.0E-31// 198aa// 37%//  
 P23144  
 SYNOV2016124  
 SYNOV2017055  
 15 SYNOV2018921  
 SYNOV2021320// SH3 DOMAIN-BINDING PROTEIN 3BP-2.// 2.3E-238// 429aa// 98%//  
 P78314  
 SYNOV3000231// Ig gamma-1 chain C region.// 0// 315aa// 95%// P01857  
 SYNOV3000302// Ig gamma-1 chain C region.// 1.00E-173// 294aa// 89%// P01857  
 20 SYNOV4000472  
 SYNOV4000706// B cell phosphoinositide 3-kinase adaptor [Mus musculus]// 0//  
 633aa// 79%// NM\_031376  
 SYNOV4001326  
 SYNOV4001395  
 25 SYNOV4002346  
 SYNOV4002392  
 SYNOV4002883// S-adenosylmethionine decarboxylase proenzyme (EC 4.1.1.50)  
 (AdoMetDC) (SamDC) [Contains: S-adenosylmethionine decarboxylase alpha chain;  
 S-adenosylmethionine decarboxylase beta chain].// 4.00E-72// 129aa// 99%//  
 30 P17707  
 SYNOV4003322  
 SYNOV4004184  
 SYNOV4004741// BENE protein (Fragment).// 2.00E-77// 140aa// 94%// Q13021  
 SYNOV4004823  
 35 SYNOV4004914  
 SYNOV4006256

SYNOV4007012  
 SYNOV4007215  
 SYNOV4007360// SSXT protein (SYT protein).// 5.00E-24// 70aa// 36%// Q62280  
 SYNOV4007430  
 5 SYNOV4007521// fibroblast growth factor receptor-like 1 precursor [Homo  
 sapiens]// 7.00E-11// 53aa// 29%// NM\_021923  
 SYNOV4007553// toll-like receptor2 [Homo sapiens]// 0// 740aa// 94%//  
 NM\_003264  
 SYNOV4007671// Syntaxin 3.// 1.00E-144// 262aa// 99%// Q13277  
 10 SYNOV4008336  
 SYNOV4008440// Protein BAP28.// 0// 1119aa// 85%// Q9H583  
 T1ESE2000116  
 TBAES2001171  
 TBAES2001220  
 15 TBAES2001229// 60S ribosomal protein L23a.// 8.00E-48// 92aa// 82%// P29316  
 TBAES2001258// SERINE PROTEASE HEPsin (EC 3.4.21.-) (TRANSMEMBRANE PROTEASE,  
 SERINE 1).// 6.40E-19// 55aa// 87%// P05981  
 TBAES2001492  
 TBAES2001751  
 20 TBAES2002197  
 TBAES2003550  
 TBAES2004055// NY-REN-50 antigen// 1.00E-155// 290aa// 99%// AAD42878.  
 TBAES2005157  
 TBAES2005543  
 25 TBAES2006568  
 TBAES2007964  
 TCERX2000613  
 TCOLN2002278  
 TESOP1000127  
 30 TESOP2000801// PROTO-ONCOGENE TYROSINE-PROTEIN KINASE YES (EC 2.7.1.112)  
 (P61-YES) (C-YES).// 3.9E-46// 159aa// 57%// Q04736  
 TESOP2001122// Caenorhabditis elegans LIN-9S (lin-9) mRNA, complete cds.//  
 5.60E-25// 222aa// 28%// AF269694  
 TESOP2001166// Mus musculus SOCS-5 mRNA, complete cds.// 1.2E-114// 439aa//  
 35 53%// AF033187  
 TESOP2001345

- TESOP2001605// Homo sapiens laryngeal carcinoma related protein 1 mRNA,  
complete cds.// 2.5E-36// 70aa// 98%// AF268387
- TESOP2001818
- TESOP2001849
- 5 TESOP2001865
- TESOP2001953// ooplasm [Mus musculus]// 7.00E-08// 58aa// 26%// NM\_011860
- TESOP2002273
- TESOP2002451
- TESOP2002489
- 10 TESOP2002539
- TESOP2002950
- TESOP2003273
- TESOP2003753
- TESOP2004114// PROCOLLAGEN-LYSINE, 2-OXOGLUTARATE 5-DIOXYGENASE 2 PRECURSOR  
15 (EC 1.14.11.4) (LYSYL HYDROXYLASE 2) (LH2).// 1.70E-202// 237aa// 99%//  
000469
- TESOP2005285// Homo sapiens partial mRNA for chr2 synaptotagmin (CHR2SYT  
gene).// 1.1E-21// 54aa// 96%// AJ303365
- TESOP2005485// Ig delta chain C region.// 2.00E-77// 136aa// 100%// P01880
- 20 TESOP2005579
- TESOP2006041
- TESOP2006060
- TESOP2006068
- TESOP2006670
- 25 TESOP2006746
- TESOP2007052
- TESOP2007262
- TESOP2007636
- TESOP2007688
- 30 TESOP2009121// Homo sapiens centromere protein E (312kD) (CENPE), mRNA//  
2.00E-10// 155aa// 20%// NM\_001813
- TESOP2009555
- TEST11000257// GLUCOSE TRANSPORTER TYPE 3, BRAIN.// 7.4E-249// 493aa// 95%//  
P11169
- 35 TEST11000319// Putative eukaryotic translation initiation factor 3 subunit  
(eIF-3) (Fragment).// 0// 683aa// 97%// 075153

TESTI1000330  
 TESTI1000348  
 TESTI1000390  
 TESTI1000491  
 5 TESTI1000545// Ring assembly protein 3.// 2.00E-14// 92aa// 26%// 074994  
 TESTI2000443  
 TESTI2000644// SMALL INDUCIBLE CYTOKINE A14 PRECURSOR (CHEMOKINE CC-1/CC-3)  
 (HCC-1/HCC-3) (NCC-2).// 2.80E-36// 69aa// 98%// Q16627  
 TESTI2002036// DIHYDROPYRIDINE-SENSITIVE L-TYPE, SKELETAL MUSCLE CALCIUM  
 10 CHANNEL ALPHA-1 SUBUNIT.// 1.70E-18// 398aa// 24%// P22316  
 TESTI2002618// ADAM 2 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE DOMAIN  
 2) (FERTILIN BETA SUBUNIT) (PH-30) (PH30).// 1.10E-57// 253aa// 47%// Q99965  
 TESTI2002928  
 TESTI2003347// Homo sapiens connexin 59 (CX59) gene, complete cds.// 1.80E-  
 15 243// 440aa// 100%// AF179597  
 TESTI2003573// Mus musculus cell cycle checkpoint control protein Mrad9 gene,  
 complete cds.// 2.4E-38// 325aa// 30%// AF045662  
 TESTI2004215// Maackia amurensis early nodulin (ENOD2) mRNA, partial cds.//  
 1.3E-34// 390aa// 31%// AF039708  
 20 TESTI2004700  
 TESTI2005376  
 TESTI2005610// H. sapiens encoding CLA-1 mRNA.// 5.9E-234// 425aa// 99%//  
 Z22555  
 TESTI2005739// Drosophila melanogaster Rho-kinase (Rhk) mRNA, complete cds.//  
 25 1.7E-09// 383aa// 24%// AF151375  
 TESTI2005986  
 TESTI2006041  
 TESTI2006643  
 TESTI2006648// ATP-binding cassette, sub-family C, member 5a// 9E-109//  
 30 452aa// 39%// NP\_038818  
 TESTI2009474  
 TESTI2009477// TRICHOHYALIN.// 1.9E-18// 124aa// 39%// P37709  
 TESTI2009511  
 TESTI2009812  
 35 TESTI2010400  
 TESTI2013381

- TESTI2013382  
 TESTI2014716// G-RICH SEQUENCE FACTOR-1 (GRSF-1).// 2.6E-228// 391aa// 99%//  
 Q12849  
 TESTI2014843
- 5 TESTI2016046// Homo sapiens HOTTTL protein mRNA, complete cds.// 2.8E-20//  
 242aa// 26%// AF078842  
 TESTI2017727  
 TESTI2018838  
 TESTI2019042
- 10 TESTI2019648  
 TESTI2023254  
 TESTI2023599  
 TESTI2024567// METABOTROPIC GLUTAMATE RECEPTOR 8 PRECURSOR.// 1.10E-130//  
 243aa// 99%// 000222
- 15 TESTI2026505// PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO/RAC  
 GEF) (FACIOGENITAL DYSPLASIA PROTEIN).// 1.40E-50// 378aa// 29%// P98174  
 TESTI2027019// Homo sapiens leucine-rich repeat-containing G protein-coupled  
 receptor 6 (LGR6) mRNA, partial cds.// 4.80E-125// 137aa// 100%// AF190501  
 TESTI2031529
- 20 TESTI2034520// Rattus norvegicus SMC (segregation of mitotic chromosomes 1)-  
 like 1 (yeast) (Smc111), mRNA// 1.00E-145// 250aa// 53%// NM\_031683  
 TESTI2034749  
 TESTI2034767// Homo sapiens collagen type IX alpha 1 chain (COL9A1) gene,  
 long and short alternatively spliced forms, exon 38 and complete cds.//  
 1.40E-191// 484aa// 73%// AF036130
- 25 TESTI2034953// Homo sapiens 88-kDa Golgi protein (GM88) mRNA, complete cds.//  
 2.00E-27// 91aa// 64%// AF204231  
 TESTI2034997  
 TESTI2035107
- 30 TESTI2035997  
 TESTI2036513  
 TESTI2036684  
 TESTI2037643  
 TESTI2040018// Homo sapiens ZNF258 (ZNF258) mRNA, complete cds.// 7.80E-97//  
 461aa// 49%// AF055470
- 35 TESTI2042450

TESTI2044796// ring finger protein 3 [Homo sapiens]// 9.00E-41// 92aa// 38%//  
NM\_006315  
TESTI2044833  
TESTI2045920  
5 TESTI2045983  
TESTI2046347  
TESTI2047071  
TESTI2048465  
TESTI2048603  
10 TESTI2048898  
TESTI2049206  
TESTI2049246  
TESTI2049277  
TESTI2049422  
15 TESTI2049452  
TESTI2049469  
TESTI2049576  
TESTI2049857// golgi stacking protein homolog GRASP55 [Rattus norvegicus]//  
5.00E-163// 410aa// 89%// AAD55350  
20 TESTI2050137// SHC transforming protein.// 1.00E-113// 232aa// 54%// P98083  
TESTI2050681  
TESTI2050987// RET finger protein-like 1.// 4.00E-35// 94aa// 34%// 075677  
TESTI2051279  
TESTI2051488  
25 TESTI2051543  
TESTI2051767  
TESTI2051806  
TESTI2051867// 60S ribosomal protein L4 (L1).// 1.00E-126// 222aa// 86%//  
P36578  
30 TESTI2052211  
TESTI2052693// brk kinase substrate [Homo sapiens].// 0// 341aa// 87%//  
CAB65105  
TESTI2052698  
TESTI2052822  
35 TESTI2053242

- TESTI2053399// Homo sapiens pescadillo homolog 1, containing BRCT domain (zebrafish) (PES1), mRNA// 9.00E-33// 63aa// 100%// NM\_014303
- TESTI2053526
- 5 TESTI2053621// Guanylyl cyclase activating protein 1 (GCAP 1) (Guanylate cyclase activator 1A).// 7.00E-96// 170aa// 92%// P43080
- TESTI4000014// 130 kDa leucine-rich protein (LRP-130) (GP130).// 0// 1210aa// 96%// P42704
- TESTI4000068
- 10 TESTI4000079// nuclear dual-specificity phosphatase [Homo sapiens]// 6.00E-07// 80aa// 36%// AAC39675
- TESTI4000209// Homo sapiens F-BOX domain protein mRNA, complete cds.// 5.5E-103// 194aa// 99%// AF248640
- TESTI4000215
- TESTI4000250
- 15 TESTI4000288// Dynamin-1 (EC 3.6.1.50) (D100) (Dynamin, brain) (B-dynamin).// 2.00E-13// 38aa// 77%// P21575
- TESTI4000349// thyroid hormone receptor interactor 12// 1.00E-39// 180aa// 40%// NP\_004229
- TESTI4000462
- 20 TESTI4000530
- TESTI4000724// solute carrier family 16 (monocarboxylic acid transporters)// 5.00E-47// 490aa// 28%// NP\_004687
- TESTI4000970
- 25 TESTI4001100// protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 1 [Homo sapiens]// 3.00E-21// 50aa// 40%// NM\_003626
- TESTI4001106// ubiquitin-protein ligase e3 component n-recognin [Mus musculus]// 1.00E-124// 228aa// 45%// NM\_009461
- TESTI4001148// Dynein beta chain, ciliary.// 1.00E-152// 282aa// 45%// P39057
- 30 TESTI4001176// Regulator of nonsense transcripts 1 (Nonsense mRNA reducing factor 1) (NORF1) (Up-frameshift suppressor 1 homolog).// 3.00E-46// 90aa// 92%// Q92900
- TESTI4001201
- TESTI4001206
- 35 TESTI4001527// UDP-glucuronosyltransferase 2C1 microsomal (EC 2.4.1.17) (UDPGT) (Fragment).// 9.00E-24// 64aa// 36%// P36514



TESTI4001561// 1-acyl-sn-glycerol-3-phosphate acyltransferase gamma (EC 2.3.1.51) (1- AGP acyltransferase 3) (1-AGPAT 3) (Lysophosphatidic acid acyltransferase-gamma) (LPAAT-gamma) (1-acylglycerol-3-phosphate O-acyltransferase 3).// 0// 319aa// 93%// Q9NRZ7

5 TESTI4001665  
TESTI4001923  
TESTI4002290  
TESTI4002491// Beta-soluble NSF attachment protein (SNAP-beta) (N-ethylmaleimide- sensitive factor attachment protein, beta) (Brain protein 147) (Fragment).// 1.00E-52// 99aa// 93%// P28663

10 TESTI4002552// Sodium/potassium-transporting ATPase alpha-4 chain (EC 3.6.3.9) (Sodium pump 4) (Na<sup>+</sup>/K<sup>+</sup> ATPase 4) (Fragment).// 0// 505aa// 94%// Q13733  
TESTI4002647

15 TESTI4002703  
TESTI4002754  
TESTI4002878  
TESTI4004200  
TESTI4005628

20 TESTI4005805  
TESTI4005857  
TESTI4005961  
TESTI4006053  
TESTI4006079// MUF1 protein; likely ortholog of mouse MUF1; elongin BC-interacting leucine-rich repeat protein [Homo sapiens]// 0// 365aa// 80%// NM\_006369  
TESTI4006112  
TESTI4006137  
TESTI4006148// putative NADH oxidoreductase complex I subunit// 2.00E-18// 40aa// 56%// AAD37863.

30 TESTI4006219  
TESTI4006326  
TESTI4006393// neural specific sr protein NSSR 2 [Mus musculus]// 7.00E-19// 70aa// 80%// BAA35093

35 TESTI4006412

- TESTI4006420// SH3-domain binding protein 5 (BTK-associated): SH3 binding protein [Homo sapiens]// 8.00E-25// 61aa// 41%// NM\_004844
- TESTI4006546// colon cancer antigen NY-CO-45 [Homo sapiens].// 0// 723aa// 99%// AAC18034
- 5 TESTI4006802// mesothelin; megakaryocyte potentiating factor [Mus musculus]// 2.00E-06// 92aa// 23%// NM\_018857
- TESTI4006819// Alpha enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (NON- neural enolase) (NNE) (Phosphopyruvate hydratase).// 1.00E-33// 72aa// 66%// P06733
- 10 TESTI4007064
- TESTI4007163// Sodium- and chloride-dependent creatine transporter 2 (CT2) (Fragment).// 2.00E-92// 153aa// 84%// P53796
- TESTI4007203
- TESTI4007239
- 15 TESTI4007373
- TESTI4007382
- TESTI4007404
- TESTI4007489
- TESTI4007775
- 20 TESTI4007778// Alpha-actinin 3 (Alpha actinin skeletal muscle isoform 3) (F-actin cross linking protein).// 0// 853aa// 94%// Q08043
- TESTI4007799
- TESTI4007810// DNA ligase III (EC 6.5.1.1) (Polydeoxyribonucleotide synthase [ATP]).// 1.00E-112// 197aa// 86%// P49916
- 25 TESTI4008007
- TESTI4008018// DAZ associated protein 2; KIAA0058 gene product [Homo sapiens]// 6.00E-41// 82aa// 75%// NM\_014764
- TESTI4008050// Translocation protein SEC63 homolog.// 1.00E-175// 314aa// 82%// Q9UGP8
- 30 TESTI4008219
- TESTI4008401
- TESTI4008429// Probable cation-transporting ATPase 2 (EC 3.6.3.-) (CGI-152).// 1.00E-136// 249aa// 94%// Q9HD20
- TESTI4008573
- 35 TESTI4008797
- TESTI4008816

TESTI4008935  
 TESTI4008993  
 TESTI4009022  
 TESTI4009034  
 5 TESTI4009123  
 TESTI4009160// Kinesin-like protein KIF2.// 6.00E-06// 39aa// 37%// P28740  
 TESTI4009215  
 TESTI4009283  
 TESTI4009286// Homo sapiens HOTTTL protein mRNA, complete cds// 2.00E-78//  
 10 180aa// 96%// AF078842  
 TESTI4009374// Apobec-1 complementation factor; APOBEC-1 stimulating protein;  
 apobec-1 complementation factor [Homo sapiens]// 1.00E-120// 203aa// 68%//  
 NM\_014576  
 TESTI4009406  
 15 TESTI4009457// p53-inducible p53DINP1 [Homo sapiens]// 3.00E-80// 140aa//  
 88%// NM\_033285  
 TESTI4009563// testis specific ankyrin-like protein 1 [Homo sapiens]// 1.00E-  
 140// 239aa// 94%// NM\_017844  
 TESTI4009608// putative T1/ST2 receptor binding protein [Homo sapiens]//  
 20 1.00E-41// 125aa// 57%// NP\_006849  
 TESTI4009638  
 TESTI4009881// Dynein heavy chain, cytosolic (DYHC) (Cytoplasmic dynein heavy  
 chain).// 5.00E-30// 176aa// 21%// Q9JHU4  
 TESTI4010211  
 25 TESTI4010377  
 TESTI4010713  
 TESTI4010789  
 TESTI4010817  
 TESTI4010831// yeast Sec31p homolog; ABP125 [Homo sapiens]// 0// 780aa//  
 30 81%// NM\_016211  
 TESTI4010851// Probable ubiquitin carboxyl-terminal hydrolase FAF-X (EC  
 3.1.2.15) (Ubiquitin thiolesterase FAF-X) (Ubiquitin-specific processing  
 protease FAF-X) (Deubiquitinating enzyme FAF-X) (Fat facets protein related,  
 X-linked) (Ubiquitin-specific protease 9, X chromosome).// 2.00E-67// 213aa//  
 35 25%// Q93008  
 TESTI4010928

TESTI4011118  
 TESTI4011161  
 TESTI4011246  
 TESTI4011484// Sec23-interacting protein p125 [Homo sapiens]// 0// 387aa//  
 5 52%// NM\_007190  
 TESTI4011505  
 TESTI4011745// WD-repeat protein 9 (Fragment).// 0// 674aa// 82%// Q9NSI6  
 TESTI4011956// Ciliary dynein heavy chain (Axonemal dynein heavy chain)  
 (Dynein heavy chain 9).// 1.00E-170// 340aa// 39%// Q9NYC9  
 10 TESTI4012086  
 TESTI4012329  
 TESTI4012406// Apolipoprotein(A) (EC 3.4.21.-) (Apo(A)) (LP(A)) (Fragment).//  
 2.00E-25// 50aa// 79%// P14417  
 TESTI4012448// Stromelysin-3 precursor (EC 3.4.24.-) (Matrix  
 15 metalloproteinase-11) (MMP-11) (ST3) (SL-3).// 0// 375aa// 99%// P24347  
 TESTI4012505// Tumor suppressor p53-binding protein 2 (p53-binding protein 2)  
 (53BP2) (Bcl2-binding protein) (Bbp).// 1.00E-81// 220aa// 34%// Q13625  
 TESTI4012556  
 TESTI4012679// Homo sapiens cryptochrome 1 (photolyase-like) (CRY1), mRNA//  
 20 0// 330aa// 97%// NM\_004075  
 TESTI4012702  
 TESTI4013369// ATP synthase lipid-binding protein, mitochondrial precursor  
 (EC 3.6.1.34) (ATP synthase proteolipid P3) (ATPase protein 9) (ATPase  
 subunit C).// 7.00E-60// 119aa// 83%// P48201  
 25 TESTI4013667  
 TESTI4013675  
 TESTI4013685  
 TESTI4013735  
 TESTI4013817// novel AMP-binding enzyme similar to acetyl-coenzyme A  
 30 synthetase (acetate-coA ligase)// 8.00E-38// 99aa// 100%// CAB75500  
 TESTI4013830// Integral membrane glycoprotein gp210 precursor.// 0// 652aa//  
 41%// P11654  
 TESTI4013924// Intracellular protein transport protein US01.// 8.00E-20//  
 125aa// 20%// P25386  
 35 TESTI4014159

TESTI4014175// Chromodomain helicase-DNA-binding protein 3 (CHD-3) (Mi-2  
 autoantigen 240 kDa protein) (Mi2-alpha).// 0// 410aa// 75%// Q12873  
 TESTI4014306  
 TESTI4014392  
 5 TESTI4014445  
 TESTI4014694  
 TESTI4014818// AD-012 protein [Homo sapiens]// 1.00E-123// 217aa// 70%//  
 NM\_018449  
 TESTI4014924// selective hybridizing clone [Mus musculus]// 0// 1153aa//  
 10 92%// NM\_011370  
 TESTI4015263  
 TESTI4015293  
 TESTI4015471  
 TESTI4015600  
 15 TESTI4015646  
 TESTI4015681  
 TESTI4015688  
 TESTI4016110// DnaJ homolog subfamily B member 8 (mDJ6).// 1.00E-91// 165aa//  
 71%// Q9QYI7  
 20 TESTI4016238  
 TESTI4016551  
 TESTI4016812  
 TESTI4016822// Protein phosphatase inhibitor 2 (IPP-2).// 9.00E-72// 133aa//  
 83%// P41236  
 25 TESTI4016882  
 TESTI4016925// Dynein beta chain, ciliary.// 0// 533aa// 34%// P39057  
 TESTI4017001  
 TESTI4017137  
 TESTI4017254  
 30 TESTI4017543// ubinuclein 1 [Homo sapiens]// 1.00E-124// 286aa// 38%//  
 NM\_016936  
 TESTI4017575  
 TESTI4017848  
 TESTI4017901// alpha-1A-adrenergic receptor, isoform 2: adrenergic, alpha -  
 35 1A-, receptor: adrenergic, alpha-1C-, receptor: alpha 1A-adrenoceptor [Homo  
 sapiens]// 9.00E-21// 51aa// 72%// NM\_033303

- TESTI4017961
- TESTI4018152// protein tyrosine phosphatase, non-receptor type 13 [Mus musculus]// 3.00E-18// 130aa// 33%// NP\_035334.
- TESTI4018208// MYOSIN IC HEAVY CHAIN.// 6.10E-07// 112aa// 40%// P10569
- 5 TESTI4018382
- TESTI4018555
- TESTI4018806
- TESTI4018835// Potential phospholipid-transporting ATPase 1K (EC 3.6.3.13) (Fragment).// 0// 514aa// 88%// 060423
- 10 TESTI4018881// early endosome antigen 1, 162kD; early endosome-associated protein [Homo sapiens]// 2.00E-14// 101aa// 22%// NM\_003566
- TESTI4018886// M-protein, striated muscle.// 4.00E-81// 146aa// 46%// Q02173
- TESTI4019140// Mi-2 histone deacetylase complex protein 66 [Xenopus laevis]// 2.00E-98// 410aa// 71%// AAD55392
- 15 TESTI4019299
- TESTI4019417
- TESTI4019566// Dosage compensation regulator (Male-less protein) (No action potential protein).// 8.00E-49// 165aa// 29%// P24785
- TESTI4019843// Rattus norvegicus huntingtin-associated protein interacting protein (duo) (Hapip), mRNA.// 0// 698aa// 91%// NM\_032062
- 20 TESTI4020092// Laminin alpha-2 chain precursor (Laminin M chain) (Merosin heavy chain).// 3.00E-40// 74aa// 96%// P24043
- TESTI4020102
- TESTI4020806
- 25 TESTI4020920
- TESTI4021294
- TESTI4021456
- TESTI4021478// Potential phospholipid-transporting ATPase 1S (EC 3.6.3.13) (Fragment).// 0// 433aa// 54%// P98196
- 30 TESTI4021491
- TESTI4022716// RNA helicase [Homo sapiens]// 0// 817aa// 95%// NM\_014314
- TESTI4022873// Dynein gamma chain, flagellar outer arm.// 3.00E-09// 106aa// 19%// Q39575
- TESTI4022936
- 35 TESTI4023546// Sialidase (EC 3.2.1.18) (Neuraminidase) (NA) (Major surface antigen).// 6.00E-32// 134aa// 23%// P23253

TESTI4023555  
 TESTI4023722  
 TESTI4023762// Trichohyalin.// 5.00E-12// 94aa// 22%// P37709  
 TESTI4023942  
 5 TESTI4024344  
 TESTI4024420// multidomain presynaptic cytomatrix protein Piccolo [Rattus norvegicus]// 0// 789aa// 82%// NM\_020098  
 TESTI4024874  
 TESTI4024890  
 10 TESTI4024907  
 TESTI4025731  
 TESTI4025797  
 TESTI4025920// B29 protein [Homo sapiens]// 2.00E-34// 73aa// 38%// NM\_031939  
 TESTI4026079  
 15 TESTI4026192  
 TESTI4026295  
 TESTI4026456  
 TESTI4026510// RNA helicase [Homo sapiens]// 0// 445aa// 89%// NM\_016130  
 TESTI4026524// Chromodomain helicase-DNA-binding protein 4 (CHD-4) (Mi-2 autoantigen 218 kDa protein) (Mi2-beta).// 0// 388aa// 59%// Q14839  
 20 TESTI4026700  
 TESTI4026762  
 TESTI4026785  
 TESTI4027516  
 25 TESTI4027557// Galectin-9 (HOM-HD-21) (Ecalectin).// 1.00E-176// 306aa// 86%// 000182  
 TESTI4027821  
 TESTI4028059// 6-phosphofructokinase, muscle type (EC 2.7.1.11) (Phosphofructokinase 1) (Phosphohexokinase) (Phosphofructo-1-kinase isozyme A) (PFK-A).// 0// 450aa// 96%// P08237  
 30 TESTI4028062  
 TESTI4028429// Eppin precursor.// 2.00E-32// 61aa// 76%// 095925  
 TESTI4028612  
 TESTI4028809  
 35 TESTI4028823// Niemann-Pick C1 protein precursor.// 6.00E-22// 127aa// 22%// P56941

- TESTI4028880// Glucose transporter type 3, brain.// 0// 436aa// 88%// P11169  
 TESTI4028983  
 TESTI4029370  
 TESTI4029671
- 5 TESTI4029836// Potential phospholipid-transporting ATPase IB (EC 3.6.3.13).//  
 0// 888aa// 93%// P98200  
 TESTI4030069// fer-1 (C.elegans)-like 3 (myoferlin); fer-1 (C. elegans)-like  
 3 [Homo sapiens]// 4.00E-22// 64aa// 38%// NM\_013451  
 TESTI4030159
- 10 TESTI4030505  
 TESTI4030603  
 TESTI4030669  
 TESTI4032895  
 TESTI4033433
- 15 TESTI4033690  
 TESTI4034172  
 TESTI4034212  
 TESTI4034432  
 TESTI4034632// polypeptide N-acetylgalactosaminyltransferase 9; UDP-GalNAc:  
 20 polypeptide N-acetylgalactosaminyltransferase 9; GalNAc transferase 9;  
 protein-UDP acetylgalactosaminyltransferase 9 [Homo sapiens]// 1.00E-113//  
 182aa// 60%// NM\_021808  
 TESTI4034912// Intracellular protein transport protein US01.// 6.00E-38//  
 219aa// 21%// P25386
- 25 TESTI4035063// Restin (Cytoplasmic linker protein-170 alpha-2) (CLIP-170)  
 (Reed- Sternberg intermediate filament associated protein).// 1.00E-17//  
 72aa// 27%// P30622  
 TESTI4035065  
 TESTI4035498// Septin-like protein KIAA0202 (Fragment).// 7.00E-58// 112aa//  
 30 49%// Q92599  
 TESTI4035602  
 TESTI4035637  
 TESTI4035649  
 TESTI4036042
- 35 TESTI4036909// Regulator of nonsense transcripts 1 homolog.// 9.00E-50//  
 140aa// 32%// Q9FJRO



TESTI4037066  
TESTI4037156// WHSC2 protein [Homo sapiens]// 0// 425aa// 80%// NM\_005663  
TESTI4037188  
TESTI4037244  
5 TESTI4037727// Dynein beta chain, ciliary.// 0// 573aa// 73%// P39057  
TESTI4038156  
TESTI4038223  
TESTI4038258  
TESTI4038339  
10 TESTI4038492  
TESTI4038818  
TESTI4039038  
TESTI4039086  
TESTI4039659// DnaJ homolog subfamily B member 8 (mDJ6).// 1.00E-91// 165aa//  
15 71%// Q9QYI7  
TESTI4040363// Surfeit locus protein 5.// 3.00E-62// 120aa// 100%// Q15528  
TESTI4040800  
TESTI4040939  
TESTI4040956  
20 TESTI4041053  
TESTI4041099  
TESTI4041143  
TESTI4041519  
TESTI4041624  
25 TESTI4041903  
TESTI4041954  
TESTI4042098  
TESTI4042444  
TESTI4042711  
30 TESTI4043129  
TESTI4043203  
TESTI4043551  
TESTI4043947  
TESTI4044035  
35 TESTI4044084  
TESTI4044123

- TESTI4044186// leucine-rich, glioma inactivated 1 [Mus musculus]// 6.00E-65//  
110aa// 60%// NM\_020278
- TESTI4044234
- TESTI4044296
- 5 TESTI4044682
- TESTI4045312
- TESTI4046253
- TESTI4046282
- TESTI4046487// plexin 1 [Mus musculus]// 0// 433aa// 97%// NM\_008881
- 10 TESTI4046819// Glucoamylase S1/S2 precursor (EC 3.2.1.3) (Glucan 1,4-alpha-glucosidase) (1,4-alpha-D-glucan glucohydrolase).// 4.00E-12// 134aa// 21%//  
P08640
- TESTI4046884
- TESTI4047069
- 15 THYMU1000496// KINESIN-LIKE PROTEIN KIF1C.// 6.40E-61// 210aa// 53%// 043896
- THYMU1000600
- THYMU2000932
- THYMU2001053
- THYMU2001090
- 20 THYMU2003397
- THYMU2003632
- THYMU2003760
- THYMU2004693
- THYMU2005003
- 25 THYMU2005190
- THYMU2005303// T-CELL SURFACE GLYCOPROTEIN CD8 ALPHA CHAIN PRECURSOR (T-LYMPHOCYTE DIFFERENTIATION ANTIGEN T8/LEU-2).// 4.2E-56// 111aa// 100%//  
P01732
- THYMU2005321
- 30 THYMU2006420// TRANSCRIPTION FACTOR-LIKE PROTEIN MRGX (KIAA0026).// 2.00E-  
129// 268aa// 92%// Q15014
- THYMU2007060// Mus musculus Cdc42 GTPase-activating protein mRNA, complete  
cds.// 1.50E-37// 270aa// 40%// AF151363
- THYMU2007179
- 35 THYMU2007658
- THYMU2008282

- THYMU2008725// PROTEIN-TYROSINE PHOSPHATASE BETA PRECURSOR (EC 3.1.3.48) (R-PTP- BETA).// 5.90E-192// 358aa// 98%// P23467
- THYMU2009134
- 5 THYMU2009157// Mus musculus MRPS18b mRNA for mitochondrial ribosomal protein S18b, complete cds.// 5.00E-38// 97aa// 77%// AB049954
- THYMU2009425// OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07J.// 4.90E-46// 173aa// 53%// P30954
- THYMU2011548// olfactory receptor 67 [Mus musculus]// 2.50E-56// 307aa// 39%// NP\_038647
- 10 THYMU2011736// latent transforming growth factor beta binding protein 3// 0// 200aa// 99%// NP\_066548
- THYMU2013386// COTE1 PROTEIN.// 2.50E-25// 269aa// 28%// P81408
- THYMU2014353
- THYMU2016204
- 15 THYMU2016523
- THYMU2019210// HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-40 B\*4002 ALPHA CHAIN PRECURSOR.// 2.1E-195// 248aa// 100%// Q04826
- THYMU2019587
- THYMU2023711// Homo sapiens mRNA for immunoglobulin lambda heavy chain.// 2.50E-233// 477aa// 89%// Y14737
- 20 THYMU2023967
- THYMU2025707
- THYMU2027497// 5-HYDROXYTRYPTAMINE 3 RECEPTOR PRECURSOR (5-HT-3) (SEROTONIN-GATED ION CHANNEL RECEPTOR) (5-HT3R).// 2E-10// 186aa// 24%// P46098
- 25 THYMU2027695// Ig gamma-1 chain C region.// 1.00E-169// 295aa// 78%// P01857
- THYMU2027734// Homo sapiens SA hypertension-associated homolog (rat) (SAH), mRNA.// 2.00E-39// 72aa// 42%// NM\_005622
- THYMU2028978
- THYMU2029676
- 30 THYMU2029688
- THYMU2030068
- THYMU2030226
- THYMU2030264
- THYMU2030637
- 35 THYMU2030796
- THYMU2031046// Copine III.// 4.00E-28// 60aa// 75%// 075131

THYMU2031218  
THYMU2031258// Homo sapiens oxysterol-binding protein-related protein (ORP1)  
mRNA, complete cds.// 4.0E-45// 125aa// 64%// AF274714  
THYMU2031341  
5 THYMU2031368  
THYMU2031579  
THYMU2031847  
THYMU2031890  
THYMU2032014// src homology 3 domain-containing protein HIP-55; HIP-55  
10 protein [Homo sapiens]// 2.00E-84// 147aa// 90%// NM\_014063  
THYMU2032035  
THYMU2032080  
THYMU2032358  
THYMU2032437  
15 THYMU2032655  
THYMU2032696  
THYMU2032825// Mus musculus mRNA for Drctnnb1a, complete cds.// 2.3E-74//  
202aa// 71%// AB030242  
THYMU2033070  
20 THYMU2033079// ATP-binding cassette protein [Mus musculus].// 2.00E-53//  
105aa// 91%// AAF31421  
THYMU2033104// nuclear prelamin A recognition factor, isoform a [Homo  
sapiens]// 5.00E-34// 111aa// 47%// NP\_036468  
THYMU2033308  
25 THYMU2033787  
THYMU2033816  
THYMU2034314  
THYMU2034374// Homo sapiens MAID protein mRNA, complete cds.// 1.5E-75//  
146aa// 100%// AF113535  
30 THYMU2034647  
THYMU2035064  
THYMU2035101  
THYMU2035319// Homo sapiens RNA-binding region (RNP1, RRM) containing 2  
(RNPC2)// 0// 354aa// 81%// NM\_004902  
35 THYMU2035388  
THYMU2035400

- THYMU2035735// *Oryctolagus cuniculus* sarcolemmal associated protein-3 mRNA, complete cds.// 3.6E-154// 350aa// 90%// U21157
- THYMU2036058
- THYMU2036085
- 5 THYMU2036252
- THYMU2036265
- THYMU2036459// 240 KDA PROTEIN OF ROD PHOTORECEPTOR CNG-CHANNEL [CONTAINS: GLUTAMIC ACID-RICH PROTEIN (GARP); CYCLIC-NUCLEOTIDE-GATED CATION CHANNEL 4 (CNG CHANNEL 4) (CNG-4) (CYCLIC NUCLEOTIDE-GATED CATION CHANNEL MODULATORY SUBUNIT)].// 1.40E-13// 527aa// 24%// Q28181
- 10 THYMU2036653
- THYMU2037081
- THYMU2037208
- THYMU2037226
- 15 THYMU2037233// RNA polymerase I transcription factor RRN3 [*Homo sapiens*]// 1.00E-71// 143aa// 95%// NP\_060897
- THYMU2037348
- THYMU2037965
- THYMU2038189
- 20 THYMU2038301// *Homo sapiens* mRNA for PRP8 protein, complete cds.// 3.90E-52// 112aa// 98%// AB007510
- THYMU2038369// *Mus musculus* GTRGE022 (Gtrgeo22) mRNA, complete cds.// 1.10E-111// 262aa// 83%// AF303106
- THYMU2038615
- 25 THYMU2038636
- THYMU2038739
- THYMU2038772
- THYMU2038797// B locus C type Lectin [*Gallus gallus*]// 2.90E-15// 147aa// 34%// CAA18961
- 30 THYMU2039305// 70 KDA WD-REPEAT TUMOR-SPECIFIC ANTIGEN (FRAGMENT).// 6.90E-40// 98aa// 83%// 035828
- THYMU2039315// *Caenorhabditis elegans* LIN-9L (lin-9) mRNA, complete cds.// 8.70E-66// 444aa// 34%// AF269693
- THYMU2039350
- 35 THYMU2039411
- THYMU2039780

- THYMU2039989  
 THYMU2040140  
 THYMU2040412  
 THYMU2040824
- 5 THYMU2040975// PTB-ASSOCIATED SPLICING FACTOR (PSF).// 1.30E-08// 119aa//  
 36%// P23246  
 THYMU2041007  
 THYMU2041015// Monocarboxylate transporter 8 (MCT 8) (X-linked PEST-  
 containing transporter) (MCT 7).// 1.00E-132// 230aa// 54%// P36021
- 10 THYMU2041252  
 THYMU3000028// Rat Tamm-Horsfall protein mRNA, complete cds.// 1.3E-21//  
 253aa// 28%// M63510  
 THYMU3000036  
 THYMU3000133
- 15 THYMU3000655  
 THYMU3000826  
 THYMU3001083// Tubulin epsilon chain (Epsilon tubulin).// 5.00E-26// 58aa//  
 98%// Q9UJT0  
 THYMU3001234// Dynamin 2 (EC 3.6.1.50) (Dynamin UDNM).// 1.00E-56// 108aa//
- 20 90%// P39054  
 THYMU3001379// 116 kDa U5 small nuclear ribonucleoprotein component (U5  
 snRNP- specific protein, 116 kDa) (U5-116 kDa).// 0// 492aa// 100%// Q15029  
 THYMU3001472  
 THYMU3001991// ART-4 protein [Homo sapiens]// 2.00E-46// 88aa// 97%//
- 25 NM\_014062  
 THYMU3002452  
 THYMU3002661  
 THYMU3003212// Saccharomyces cerevisiae TAD2 gene for tRNA-specific  
 adenosine-34 deaminase subunit Tad2p.// 1.10E-21// 135aa// 40%// AJ242667
- 30 THYMU3003309// putative tumor antigen [Homo sapiens]// 2.00E-52// 105aa//  
 66%// NM\_018666  
 THYMU3003763  
 THYMU3004157// peroxisomal acyl-CoA thioesterase [Homo sapiens]// 3.00E-44//  
 85aa// 82%// NM\_005469
- 35 THYMU3004835// Probable beta-1,3-galactosyltransferase 8 (EC 2.4.1.-) (Beta-  
 1,3- GalTase 8) (Beta3Gal-T8) (b3Gal-T8) (UDP-galactose:beta-N-

- acetylglucosamine beta-1,3-galactosyltransferase 8) (UDP-Gal:beta- GlcNAc  
 beta-1,3-galactosyltransferase 8) (Beta-3-Gx-T8).// 2.00E-78// 146aa// 43%//  
 Q9Y2A9
- THYMU3004866// TPA inducible gene-1; TPA inducible protein [Homo sapiens]//  
 5 3.00E-47// 93aa// 86%// NM\_015889
- THYMU3005696
- THYMU3006118// molybdenum cofactor synthesis 2 [Homo sapiens]// 3.00E-60//  
 112aa// 100%// NM\_004531
- THYMU3006132
- 10 THYMU3006168
- THYMU3006172// membrane bound C2 domain containing protein [Rattus  
 norvegicus]// 1.00E-145// 460aa// 52%// NP\_058945
- THYMU3006371
- THYMU3006485
- 15 THYMU3006811// ATP-binding cassette, sub-family A, member 7, isoform a//  
 3.00E-11// 82aa// 41%// NP\_061985
- THYMU3006963
- THYMU3007137// Interleukin-16 precursor (IL-16) (Lymphocyte chemoattractant  
 factor) (LCF).// 0// 528aa// 83%// Q14005
- 20 THYMU3007368
- THYMU3007845
- THYMU3008171
- THYMU3008436// 6-phosphofructokinase, muscle type (EC 2.7.1.11)  
 (Phosphofructokinase 1) (Phosphohexokinase) (Phosphofructo-1-kinase isozyme  
 A) (PFK-A).// 0// 764aa// 98%// P08237
- 25 THYMU3009255
- TKIDN2000701// ankyrin G // 1.6E-90// 178aa// 100%// AAA64834
- TKIDN2002424
- TKIDN2002632
- 30 TKIDN2003044
- TKIDN2004386
- TKIDN2005934
- TKIDN2005947
- TKIDN2006525
- 35 TKIDN2006852// Homo sapiens cytosolic phospholipase A2 gamma (cPLA2 gamma)  
 mRNA, complete cds.// 4.3E-103// 192aa// 100%// AF065214

TKIDN2007667  
 TKIDN2009092  
 TKIDN2009641  
 TKIDN2009889  
 5 TKIDN2010934  
 TKIDN2012824  
 TKIDN2013287  
 TKIDN2014757  
 TKIDN2014771  
 10 TKIDN2015263  
 TKIDN2015788  
 TKIDN2016309  
 TKIDN2019116  
 TLIVE2000023  
 15 TLIVE2001327// Human DOCK180 protein mRNA, complete cds.// 0// 961aa// 63%//  
 D50857  
 TLIVE2001828  
 TLIVE2001927  
 TLIVE2002336// ectonucleotide pyrophosphatase/phosphodiesterase 5 [Mus  
 20 musculus]// 7.00E-69// 144aa// 36%// NM\_032003  
 TLIVE2002338  
 TLIVE2002690  
 TLIVE2003197  
 TLIVE2003225// CUB and Sushi multiple domains 1 [Homo sapiens]// 1.00E-129//  
 25 199aa// 58%// NM\_033225  
 TLIVE2003381// taste receptor, type 1, member 3: saccharin preference [Mus  
 musculus]// 8.00E-65// 112aa// 79%// NM\_031872  
 TLIVE2003970  
 TLIVE2004110  
 30 TLIVE2004320// Homo sapiens PC2-glutamine-rich-associated protein (PCQAP)  
 mRNA, complete cds.// 4.7E-201// 368aa// 99%// AF328769  
 TLIVE2004601  
 TLIVE2005180  
 TLIVE2006236  
 35 TLIVE2006529  
 TLIVE2007132



TLIVE2007528  
TLIVE2007816  
TLIVE2008083  
TLIVE2008229// SIGNAL RECOGNITION PARTICLE 68 KDA PROTEIN (SRP68).// 1.00E-  
5 299// 506aa// 96%// Q00004  
TLIVE2009541  
TOVAR2000649  
TOVAR2001281  
TOVAR2001730  
10 TOVAR2002247// Homo sapiens partial partial mRNA for NICE-4 protein, clone  
3114f17.// 1.0E-117// 218aa// 100%// AJ243670  
TOVAR2002549  
TRACH1000205  
TRACH2001443  
15 TRACH2001549// Homo sapiens mRNA for neuropathy target esterase.// 1.10E-94//  
295aa// 65%// AJ004832  
TRACH2001684  
TRACH2003070  
TRACH2004170  
20 TRACH2005066  
TRACH2005811  
TRACH2006049  
TRACH2006387// P2Y PURINOCEPTOR 1 (ATP RECEPTOR) (P2Y1) (PURINERGIC  
RECEPTOR).// 2E-56// 307aa// 36%// P49650  
25 TRACH2007059// Folate hydrolase (Prostate-specific membrane antigen 1).//  
2.00E-37// 127aa// 26%// Q04609  
TRACH2007834  
TRACH2008300  
TRACH2009310// PUTATIVE SERINE/THREONINE-PROTEIN KINASE D1044.3 IN CHROMOSOME  
30 III (EC 2.7.1.-).// 9.40E-85// 407aa// 38%// P41951  
TRACH2019248  
TRACH2019473  
TRACH2020525  
TRACH2021398  
35 TRACH2021964  
TRACH2022042

TRACH2022425// Ig alpha-1 chain C region.// 0// 319aa// 91%// P01876  
 TRACH2022553// Human germline IgD-chain gene, C-region, second domain of  
 membrane terminus.// 1.70E-234// 429aa// 99%// K02882  
 TRACH2022649// Ig gamma-1 chain C region.// 0// 315aa// 95%// P01857  
 5 TRACH2023299// growth factor receptor bound protein 2-associated protein 2  
 [Mus musculus]// 5.00E-40// 77aa// 58%// NM\_010248  
 TRACH2023306  
 TRACH2025344  
 TRACH2025507// tumor suppressing subtransferable candidate 1; tumor-  
 10 supressing STF cDNA 1 [Homo sapiens]// 4.00E-48// 87aa// 74%// NM\_003310  
 TRACH2025535// evecin-2 [Mus musculus]// 2.00E-75// 230aa// 90%// AAF01332  
 TRACH2025749  
 TRACH2025911  
 TRACH2025932  
 15 TRACH3000014  
 TRACH3000342  
 TRACH3000558// CREB-BINDING PROTEIN.// 1.9E-90// 120aa// 100%// Q92793  
 TRACH3000586  
 TRACH3000926// cardiac morphogenesis [Mus musculus]// 0// 417aa// 63%//  
 20 NM\_011724  
 TRACH3001427// p47 [Homo sapiens]// 2.00E-85// 167aa// 49%// NM\_016143  
 TRACH3002064  
 TRACH3002168// Cell surface glycoprotein MUC18 precursor (Melanoma-associated  
 antigen MUC18) (Melanoma-associated antigen A32) (S-endo 1 endothelial-  
 25 associated antigen) (CD146 antigen) (Melanoma adhesion molecule).// 0//  
 341aa// 94%// P43121  
 TRACH3002192  
 TRACH3002650  
 TRACH3002866  
 30 TRACH3002871  
 TRACH3003379  
 TRACH3004068  
 TRACH3004537  
 TRACH3004721// 80 kda MCM3-associated protein (GANP protein).// 0// 474aa//  
 35 77%// 060318

- TRACH3004786// Claudin-4 (Clostridium perfringens enterotoxin receptor) (CPE-receptor) (CPE-R).// 2.00E-90// 162aa// 77%// 014493  
 TRACH3004840  
 TRACH3005294
- 5 TRACH3005479  
 TRACH3005549// Ig heavy chain V region IR2 precursor.// 4.00E-47// 89aa// 61%// P01805  
 TRACH3006038  
 TRACH3006149
- 10 TRACH3006228  
 TRACH3006412// Homo sapiens COP9 constitutive photomorphogenic homolog subunit 7B// 3.00E-57// 105aa// 99%// NM\_022730  
 TRACH3006470  
 TRACH3006889
- 15 TRACH3007391  
 TRACH3007479// Nedd-4-like ubiquitin-protein ligase; WW domain-containing protein 2 [Homo sapiens]// 0// 320aa// 93%// NM\_007014  
 TRACH3008093  
 TRACH3008535
- 20 TRACH3008629// Cadherin-related tumor suppressor homolog precursor (Fat protein homolog).// 6.00E-36// 143aa// 28%// Q14517  
 TRACH3008713// Beta-soluble NSF attachment protein (SNAP-beta) (N-ethylmaleimide-sensitive factor attachment protein, beta) (Brain protein 147) (Fragment).// 4.00E-52// 98aa// 92%// P28663
- 25 TRACH3009455// Phosphatidylinositol 3-kinase regulatory alpha subunit (PI3-kinase P85-alpha subunit) (PtdIns-3-kinase P85-alpha) (PI3K).// 0// 386aa// 95%// P27986  
 TRACH3034731// Ras association (RalGDS/AF-6) domain family 2// 7.00E-56// 320aa// 40%// NP\_055552
- 30 TRACH3034762  
 TRACH3035199// antigen identified by monoclonal antibody MRC OX-2 receptor [Rattus norvegicus]// 1.00E-86// 170aa// 51%// NM\_023953  
 TRACH3035235  
 TRACH3035482
- 35 TRACH3035526// Ig alpha-2 chain C region.// 0// 324aa// 95%// P01877

TRACH3036193// Genome polyprotein [Contains: Coat proteins VP1 TO VP4; Core proteins P2A TO P2C, P3A; Genome-linked protein VPG; Picornain 3C (EC 3.4.22.28) (Protease 3C) (P3C); RNA-directed RNA polymerase P3D (EC 2.7.7.48)].// 0// 1073aa// 69%// Q82122

5 TRACH3036207

TRACH3036309

TRACH3036456

TRACH3036609// J kappa-recombination signal binding protein (RBP-J kappa).// 1.00E-158// 271aa// 89%// P31266

10 TSTOM1000135

TSTOM2000442// Ig gamma-1 chain C region.// 1.00E-168// 292aa// 77%// P01857

TSTOM2000553// SYNAPTOTAGMIN IV.// 3.00E-08// 150aa// 28%// P40749

TSTOM2002672

TUTER1000122

15 TUTER2000425// zinc finger protein SBZF3 [Homo sapiens]// 4.00E-36// 74aa// 81%// NM\_020394

TUTER2000904// Unc-119 protein homolog (Retinal protein 4) (RRG4).// 7.00E-72// 129aa// 70%// Q62885

TUTER2000916

20 TUTER2001387

TUTER2002729// D6MM5E protein [Mus musculus]// 1.00E-107// 191aa// 68%// NM\_033079

UTERU1000024

UTERU1000031// G.gallus mRNA for tom-1B protein.// 2.1E-149// 535aa// 59%//

25 Y08741

UTERU1000148

UTERU1000249

UTERU1000337// Putative protein phosphatase 2C (EC 3.1.3.16) (PP2C).// 1.00E-156// 271aa// 94%// P49593

30 UTERU1000339

UTERU2000649

UTERU2001409

UTERU2002410

UTERU2002841

35 UTERU2004688

UTERU2004929

UTERU2005004  
 UTERU2005621// CDC14 homolog B, isoform 2 [Homo sapiens]// 0// 423aa// 94%//  
 NM\_033331  
 UTERU2006115// ALPHA-ADAPTIN A (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-A  
 5 LARGE CHAIN) (100 KDA COATED VESICLE PROTEIN A) (PLASMA MEMBRANE ADAPTOR  
 HA2/AP2 ADAPTIN ALPHA A SUBUNIT).// 9.0E-141// 268aa// 99%// P17426  
 UTERU2006137  
 UTERU2006568  
 UTERU2007444  
 10 UTERU2007520  
 UTERU2007724// Calponin H2, smooth muscle (Neutral calponin).// 1.00E-144//  
 253aa// 86%// Q99439  
 UTERU2008347// Chlamydomonas reinhardtii vegetative cell wall protein gp1  
 (GP1) gene, complete cds.// 1.0E-19// 199aa// 30%// AF309494  
 15 UTERU2014678  
 UTERU2017762// plexin B1; KIAA0407 protein; plexin 5 [Homo sapiens]// 0//  
 383aa// 60%// NM\_002673  
 UTERU2019491// Homo sapiens mRNA for 41-kDa phosphoribosylpyrophosphate  
 synthetase-associated protein, complete cds.// 4.30E-48// 101aa// 100%//  
 20 AB007851  
 UTERU2019681  
 UTERU2019706// T-COMPLEX PROTEIN 1, GAMMA SUBUNIT (TCP-1-GAMMA) (CCT-  
 GAMMA).// 9.80E-273// 426aa// 99%// P49368  
 UTERU2019940// mitochondrial ribosomal protein L30 [Homo sapiens]// 2.00E-  
 25 44// 82aa// 97%// NM\_016503  
 UTERU2020491  
 UTERU2020718  
 UTERU2021163  
 UTERU2021380  
 30 UTERU2022020  
 UTERU2022981  
 UTERU2023039  
 UTERU2023175  
 UTERU2023651  
 35 UTERU2023712  
 UTERU2024002

- UTERU2024656  
 UTERU2025025// High affinity nerve growth factor receptor precursor (EC 2.7.1.112) (TRK1 transforming tyrosine kinase protein) (p140-TrkA) (Trk-A).// 0// 479aa// 95%// P04629
- 5 UTERU2025645  
 UTERU2025891  
 UTERU2026025// SPLICING FACTOR, ARGININE/SERINE-RICH 2 (SPLICING FACTOR SC35) (SC-35) (SPLICING COMPONENT, 35 KDA) (PR264 PROTEIN).// 8.00E-30// 61aa// 100%// P30352
- 10 UTERU2026090// Cartilage-associated protein precursor.// 1.00E-180// 309aa// 87%// 075718  
 UTERU2026203// phosphoinositide phosphatase SAC1 [Rattus norvegicus].// 1.00E-107// 221aa// 95%// AAG29810  
 UTERU2027591// calcium-activated potassium channel // 7.8E-33// 79aa// 94%//
- 15 AAA50216  
 UTERU2029953  
 UTERU2030213  
 UTERU2030280  
 UTERU2031084
- 20 UTERU2031268// NY-REN-25 antigen [Homo sapiens].// 1.00E-41// 330aa// 49%// AAD42869  
 UTERU2031521  
 UTERU2031703  
 UTERU2031851
- 25 UTERU2033375  
 UTERU2033382  
 UTERU2035114  
 UTERU2035323  
 UTERU2035328// Homo sapiens putative transcription factor CA150 mRNA, complete cds.// 1.80E-271// 796aa// 70%// AF017789
- 30 UTERU2035331  
 UTERU2035452// NG3 [Homo sapiens]// 1.00E-136// 150aa// 99%// AAB47494  
 UTERU2035469// Mus musculus microfibril-associated glycoprotein-2 (Magp2) mRNA, complete cds.// 1.2E-52// 164aa// 66%// AF180805
- 35 UTERU2035503

- UTERU2035745// MYOSIN IA HEAVY CHAIN (MYOSIN-LIKE PROTEIN ABMA).// 1.30E-11//  
101aa// 31%// P22467
- UTERU2036089// SH3-BINDING PROTEIN 3BP-1.// 4.1E-168// 369aa// 86%// P55194
- UTERU2037361
- 5 UTERU2037577
- UTERU2038251
- UTERU3000226
- UTERU3000645// Claudin-4 (Clostridium perfringens enterotoxin receptor) (CPE-  
receptor) (CPE-R).// 3.00E-89// 161aa// 77%// 014493
- 10 UTERU3000665// Snf2-related CBP activator protein [Homo sapiens].// 7.00E-  
59// 500aa// 97%// NP\_006653
- UTERU3000828// 116 kDa U5 small nuclear ribonucleoprotein component (U5  
snRNP- specific protein, 116 kDa)--(U5-116 kDa).// 0// 931aa// 95%// Q15029
- UTERU3000899// hTGN51 [Homo sapiens].// 1.00E-101// 281aa// 72%// AAC39542
- 15 UTERU3001059// ABC1 protein homolog, mitochondrial precursor.// 2.00E-99//  
188aa// 48%// Q92338
- UTERU3001240// Adenylate cyclase, type IV (EC 4.6.1.1) (ATP pyrophosphate-  
lyase) (Adenylyl cyclase).// 1.00E-176// 308aa// 81%// P26770
- UTERU3001542
- 20 UTERU3001571
- UTERU3001572// Neuroblast differentiation associated protein AHNAK  
(Desmoyokin) (Fragments).// 6.00E-19// 213aa// 21%// Q09666
- UTERU3001585// Cytochrome P450 4c3 (EC 1.14.-.-) (CYP1VC3).// 1.00E-125//  
230aa// 49%// Q9VA27
- 25 UTERU3001652// 64 KDA AUTOANTIGEN D1 (THYROID-ASSOCIATED OPHTHALMOPATHY  
AUTOANTIGEN).// 1.00E-219// 416aa// 99%// P29536
- UTERU3001766
- UTERU3001988// COATOMER EPSILON SUBUNIT (EPSILON-COAT PROTEIN) (EPSILON-  
COP).// 1.70E-126// 159aa// 94%// Q28104
- 30 UTERU3002209
- UTERU3002218
- UTERU3002383
- UTERU3002667
- UTERU3002731
- 35 UTERU3002768
- UTERU3002786

UTERU3002993

UTERU3003116// ADAM 12 precursor (EC 3.4.24.-) (A disintegrin and metalloproteinase domain 12) (Meltrin alpha).// 1.00E-20// 48aa// 44%// 043184

5 UTERU3003135// Splicing factor 3B subunit 2 (Spliceosome associated protein 145) (SAP 145) (SF3b150) (Pre-mRNA splicing factor SF3b 145 kDa subunit).// 6.00E-29// 62aa// 83%// Q13435

UTERU3003178// Kinesin light chain 2 (KLC 2).// 0// 312aa// 88%// Q9H0B6  
UTERU3003465

10 UTERU3003523

UTERU3003776

UTERU3004523

UTERU3004616

UTERU3004709

15 UTERU3004992// Aortic preferentially expressed protein 1 (APEG-1).// 3.00E-61// 113aa// 100%// Q15772

UTERU3005049

UTERU3005205

UTERU3005230

20 UTERU3005460

UTERU3005585// rhophilin-like protein [Homo sapiens]// 0// 380aa// 91%// NM\_033103

UTERU3005907// PROTEIN-GLUTAMINE GAMMA-GLUTAMYLTRANSFERASE (EC 2.3.2.13) (TISSUE TRANSGLUTAMINASE) (TGASE C) (TGC) (TGASE-H).// 1.30E-75// 152aa//

25 98%// P21980

UTERU3005970

UTERU3006008

UTERU3006308// SEMAPHORIN 4C PRECURSOR (SEMAPHORIN I) // 1.00E-128// 330aa// 86%// Q64151

30 UTERU3007134

UTERU3007419// Rattus norvegicus Ca<sup>2+</sup>-dependent activator protein (CAPS) mRNA, complete cds.// 0// 1223aa// 78%// U16802

UTERU3007640// N-ethylmaleimide-sensitive factor attachment protein, alpha:// 5.00E-54// 110aa// 87%// NP\_003818

35 UTERU3007913

UTERU3008660



UTERU3008671// SPARC precursor (Secreted protein acidic and rich in cysteine)  
 (Osteonectin) (ON) (Basement membrane protein BM-40).// 4.00E-25// 49aa//  
 96%// P09486  
 UTERU3009259  
 5 UTERU3009490// LYSP100 protein (Lymphoid-restricted homolog of Sp100)  
 (Nuclear autoantigen Sp-140) (Speckled 140 kDa) (Nuclear body protein  
 Sp140).// 4.00E-33// 67aa// 61%// Q13342  
 UTERU3009517  
 UTERU3009690// alpha-1A-adrenergic receptor, isoform 2: adrenergic, alpha -  
 10 1A-, receptor: adrenergic, alpha-1C-, receptor: alpha 1A-adrenoceptor [Homo  
 sapiens]// 5.00E-16// 41aa// 67%// NM\_033303  
 UTERU3009871// feminization 1 homolog a (C. elegans)// 0// 588aa// 85%//  
 NP\_034322  
 UTERU3009979// growth arrest-specific 6: AXL stimulatory factor [Homo  
 15 sapiens]// 0// 572aa// 97%// NM\_000820  
 UTERU3011063// Transmembrane 9 superfamily protein member 4.// 0// 402aa//  
 89%// Q92544  
 UTERU3015086  
 UTERU3015500// G protein-coupled receptor 49// 1.00E-15// 350aa// 29%//  
 20 NP\_003658  
 UTERU3016789// SH3 domain-binding protein 3BP-2.// 1.00E-146// 261aa// 75%//  
 P78314  
 UTERU3018081  
 UTERU3018154  
 25 UTERU3018616  
 UTERU3018711  
 3NB692004724  
 ADRGL2000042// Homo sapiens CTCL tumor antigen se20-4 mRNA, complete cds.//  
 6.20E-143// 269aa// 100%// AF273046  
 30 ADRGL2000056  
 BLADE2000579  
 BLADE2006830  
 BRACE2002589  
 BRACE2003609// endothelial zinc finger protein induced by tumor necrosis  
 35 factor alpha [Homo sapiens]// 0// 310aa// 67%// NM\_021216  
 BRACE2009318

BRACE2011677  
 BRACE2029396  
 BRACE2037299  
 BRACE2039823// CDP-DIACYLGLYCEROL—INOSITOL 3-PHOSPHATIDYLTRANSFERASE (EC  
 5 2.7.8.11) (PHOSPHATIDYLINOSITOL SYNTHASE) (PTDINS SYNTHASE) (PI SYNTHASE).//  
 2.10E-79// 154aa// 100%// 014735  
 BRACE2039832  
 BRACE2043105  
 BRACE3001058// zinc finger protein 347; zinc finger 1111 [Homo sapiens]// 0//  
 10 382aa// 52%// NM\_032584  
 BRACE3001113// Zinc finger protein 91 (Zinc finger protein HTF10) (HPF7).//  
 6.00E-92// 226aa// 26%// Q05481  
 BRACE3003026  
 BRACE3003053  
 15 BRACE3005107// // // //  
 BRACE3009127// oxysterol binding protein 2; oxysterol binding protein-like 1  
 [Homo sapiens]// 0// 670aa// 95%// NM\_030758  
 BRACE3010076// Vigilin (High density lipoprotein-binding protein) (HDL-  
 binding protein).// 0// 464aa// 92%// Q00341  
 20 BRACE3015829  
 BRACE3021148// DC12 protein [Homo sapiens]// 1.00E-16// 60aa// 30%//  
 NM\_020187  
 BRALZ2017844// HOMEBOX PROTEIN CHOX-E (CHOX E) (FRAGMENT).// 2.80E-59//  
 157aa// 75%// Q91975  
 25 BRAMY2019111// POLYCYSTIN 2.// 6.30E-18// 204aa// 27%// 035245  
 BRAMY2035070// Homo sapiens zinc finger 1111 mRNA, complete cds.// 1.70E-  
 213// 723aa// 53%// AY029765  
 BRAMY2035449// Mus musculus zinc finger protein ZFP113 mRNA, complete cds.//  
 2.70E-95// 356aa// 44%// AF167320  
 30 BRAMY2035718// NUCLEAR FACTOR 1-B (NF1-B) (CCAAT BOX-BINDING TRANSCRIPTION  
 FACTOR) (CTF) (TGGCA-BINDING PROTEIN).// 5.60E-228// 418aa// 97%// P97863  
 BRAMY2038516// PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC  
 5.3.4.1).// 7.00E-237// 434aa// 99%// Q15084  
 BRAMY2039341// ZINC FINGER PROTEIN 135.// 7.30E-84// 227aa// 62%// P52742  
 35 BRAMY2040159// Homo sapiens MRIP-1 mRNA, complete cds.// 6.00E-234// 345aa//  
 91%// AF359283

- BRAMY2041434  
 BRAMY2045471// Homo sapiens CGI-89 protein mRNA, complete cds.// 6.00E-45//  
 147aa// 44%// CAB82308  
 BRAMY3004800// Huntingtin-associated protein-interacting protein (Duo  
 5 protein).// 0// 751aa// 91%// 060229  
 BRAWH1000369// Homo sapiens putative DNA polymerase mRNA, partial cds.//  
 5.40E-150// 199aa// 97%// AF044578  
 BRAWH2006207// ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//  
 8.90E-32// 83aa// 81%// Q05481  
 10 BRAWH2006395// transmembrane receptor UNC5H1// 1.00E-141// 292aa// 88%//  
 AAB57678  
 BRAWH2008993  
 BRAWH2009393  
 BRAWH2010552  
 15 BRAWH3007441// CAT56 protein [Homo sapiens]// 1.00E-44// 78aa// 84%//  
 NM\_025263  
 BRAWH3009017// SEL-10 protein.// 6.00E-38// 73aa// 61%// Q93794  
 BRCAN2002473// Tropomyosin, fibroblast isoform 2 (TM-2).// 1.00E-114//  
 230aa// 70%// P19354  
 20 BRCAN2002854// Human Hsp27 ERE-TATA-binding protein (HET) mRNA, complete  
 cds.// 2.60E-21// 240aa// 35%// U72355  
 BRCAN2003070// ubiquitin carrier protein E2-C [Homo sapiens]// 9.00E-51//  
 80aa// 78%// NP\_008950  
 BRCAN2014229  
 25 BRCOC2019841  
 BRHIP2002722  
 BRHIP2003272  
 BRHIP2005271// protein tyrosine phosphatase// 7.00E-39// 190aa// 42%//  
 NP\_006255  
 30 BRHIP2005724// Homo sapiens mRNA for NDRG4-B, complete cds.// 3.10E-182//  
 301aa// 98%// AB044944  
 BRHIP2006617// NUCLEAR AUTOANTIGENIC SPERM PROTEIN (NASP).// 1.20E-156//  
 313aa// 97%// P49321  
 BRHIP2008389// Drosophila melanogaster furry protein short isoform mRNA,  
 35 partial cds.// 1.70E-29// 179aa// 44%// AF351187  
 BRHIP2012360// XPG\_XENLA// 4.00E-17// 70aa// 41%// P14629

- BRHIP2017553// Zinc finger protein 184.// 1.00E-164// 272aa// 49%// Q99676  
 BRHIP2026877// Tyrosine-protein kinase receptor TYR03 precursor (EC  
 2.7.1.112) (Tyrosine-protein kinase RSE) (Tyrosine-protein kinase SKY)  
 (Tyrosine- protein kinase DTK) (Protein-tyrosine kinase byk).// 3.00E-56//  
 5 104aa// 80%// Q06418  
 BRHIP3000017  
 BRHIP3000240// Homo sapiens potassium channel beta 2 subunit (HKvbeta2.2)  
 mRNA, alternatively spliced, complete cds.// 1.70E-172// 347aa// 95%//  
 AF044253  
 10 BRHIP3008314// sirtuin 2, isoform 2: silencing information regulator 2-like;  
 sir2-like 2: silent mating type information regulation 2, S.cerevisiae,  
 homolog 2: sir2-related protein type 2 [Homo sapiens]// 2.00E-48// 86aa//  
 98%// NM\_030593  
 BRHIP3026052// Serine/threonine protein phosphatase 2A, 56 kDa regulatory  
 15 subunit, gamma isoform (PP2A, B subunit, B' gamma isoform) (PP2A, B subunit,  
 B56 gamma isoform) (PP2A, B subunit, PR61 gamma isoform) (PP2A, B subunit, R5  
 gamma isoform).// 0// 424aa// 83%// Q13362  
 BRSTN2013354// ETS-related protein PE-1 (ETS translocation variant 3)  
 (Fragment).// 4.00E-61// 109aa// 84%// P41162  
 20 BRTHA2002133  
 BRTHA2002702  
 BRTHA2007060// EUKARYOTIC TRANSLATION INITIATION FACTOR 3 SUBUNIT 10 (EIF-3  
 THETA) (EUKARYOTIC TRANSLATION INITIATION FACTOR 3 LARGE SUBUNIT) (PNLA-  
 35).// 0// 963aa// 74%// Q40554  
 25 BRTHA2010033  
 BRTHA2011321  
 BRTHA2013426  
 BRTHA2013610// deoxyguanosine kinase, putative [Arabidopsis thaliana]//  
 1.00E-142// 360aa// 78%// NP\_565032\*  
 30 BRTHA2016318// WTAP protein// 9.00E-87// 240aa// 100%// CAC10188  
 BRTHA2017364// PUTATIVE ATP-DEPENDENT RNA HELICASE T26G10.1 IN CHROMOSOME  
 III.// 1.10E-33// 207aa// 34%// P34580  
 BRTHA2017972// Homo sapiens MAD-related gene SMAD7 (SMAD7) mRNA, complete  
 cds.// 5.30E-114// 207aa// 99%// AF010193  
 35 BRTHA2018011// EPITHIN (EC 3.4.21.-).// 1.70E-53// 242aa// 45%// P56677

- BRTHA2018443// POTENTIAL PHOSPHOLIPID-TRANSPORTING ATPASE IS (EC 3.6.1.-)  
(FRAGMENT).// 3.10E-195// 581aa// 61%// P98196
- BRTHA3000296
- BRTHA3003000// apoptosis-associated tyrosine kinase [Homo sapiens]// 1.00E-  
5 161// 300aa// 64%// NM\_004920
- BRTHA3008826
- CERVX2002013// TRANSCRIPTION FACTOR BTEB2 (BASIC TRANSCRIPTION ELEMENT  
BINDING PROTEIN 2) (GC BOX BINDING PROTEIN 2).// 3.30E-33// 81aa// 81%//  
Q13887
- 10 CTONG1000113// ZINC FINGER PROTEIN 184 (FRAGMENT).// 0// 641aa// 85%// Q99676
- CTONG2003348// Mus musculus mRNA for OASIS protein, complete cds.// 9.60E-  
87// 392aa// 51%// AB017614
- CTONG2004000
- CTONG2008721// Homo sapiens CAGH44 mRNA, partial cds.// 2.70E-94// 215aa//  
15 91%// U80741
- CTONG2015596
- CTONG2015633
- CTONG2016942// Homo sapiens serine protease DESC1 (DESC1) mRNA, complete  
cds.// 2.00E-95// 425aa// 43%// AF064819
- 20 CTONG2019822
- CTONG2020374
- CTONG2020378// ZINC FINGER PROTEIN 35 (ZFP-35).// 5.70E-100// 322aa// 55%//  
P15620
- CTONG2020411// BASONUCLIN.// 1.30E-139// 616aa// 48%// Q01954
- 25 CTONG2020974// Homo sapiens mRNA for putative progesterone binding protein.//  
8.10E-118// 223aa// 100%// AJ002030
- CTONG2024031
- CTONG2028758// Mus musculus zfh-4 mRNA for zinc-finger homeodomain protein 4,  
complete cds.// 0// 907aa// 91%// AB024499
- 30 CTONG3001501// Mus musculus glucocorticoid-induced gene 1 mRNA, complete  
cds.// 3.60E-202// 413aa// 89%// AF292939
- CTONG3002552
- CTONG300359°
- CTONG3004550// SH3-domain binding protein 4 [Homo sapiens]// 1.00E-179//  
35 351aa// 42%// NM\_014521

- CTONG3004726// ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//  
4.20E-230// 663aa// 55%// Q05481
- CTONG3009287
- DFNES2011192// Homo sapiens ZNF140-like transcription factor mRNA, complete  
5 cds.// 1.10E-221// 396aa// 99%// AF326206
- FCBBF1000509// Homo sapiens mRNA for photolyase, complete cds.// 9.80E-280//  
500aa// 99%// D83702
- FCBBF3010361// Danio rerio mRNA for winged helix nude (whn gene).// 2.10E-  
107// 336aa// 64%// AJ252024
- 10 FCBBF3027854// contains similarity to Arabidopsis thaliana DNA-damage-  
repair/tolerance resistance protein DRT111 (SW:P42698// 9.60E-12// 87aa//  
37%// AAC13593
- FEBRA2000790
- FEBRA2001990// SON OF SEVENLESS PROTEIN HOMOLOG 2 (SOS-2) (MSOS-2)  
15 (FRAGMENT).// 4.00E-09// 175aa// 20%// Q02384
- FEBRA2006519// Mus musculus papilin mRNA, complete cds.// 4.90E-58// 327aa//  
37%// AF314171
- FEBRA2008692// Homo sapiens IRE1b mRNA for protein kinase/ribonuclease IRE1  
beta, complete cds.// 0// 926aa// 96%// AB047079
- 20 FEBRA2014122// wizL [Mus musculus]// 0// 661aa// 88%// BAA32790
- FEBRA2027609// ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//  
5.60E-196// 688aa// 51%// Q05481
- FEBRA2028256// FIBRILLIN 2 PRECURSOR.// 2.90E-231// 527aa// 62%// Q61555
- FEBRA2028516
- 25 HCASM2002754
- HCASM2003018// Homo sapiens nuclear transcription factor NFX2 (NFX2) mRNA,  
complete cds.// 3.90E-70// 666aa// 31%// AF332009
- HCASM2003099// HISTONE DEACETYLASE CLR3.// 5.00E-19// 108aa// 49%// P56523
- HCASM2003357
- 30 HCASM2008536// DNA-REPAIR PROTEIN XRCC1.// 2.00E-12// 119aa// 36%// P18887
- HCASM2009424// regulatory factor (trans-acting) 2 [Mus musculus]// 7.00E-24//  
60aa// 48%// NP\_033082
- HCHON2000508// Homo sapiens prostate antigen PARIS-1 mRNA, complete cds.//  
0// 686aa// 99%// AY026527
- 35 HCHON2000743

- HCHON2004858// Zinc finger protein 29 (Zfp-29).// 1.00E-124// 208aa// 60%// Q07230
- HEART2009680// Vasoactive intestinal polypeptide receptor 2 precursor (VIP-R-2) (Pituitary adenylate cyclase activating polypeptide type III receptor) (PACAP type III receptor) (PACAP-R-3) (Helodermin-preferring VIP receptor).// 0// 309aa// 96%// P41587
- 5 HLUNG2013350// Mus musculus mRNA for synaptotagmin VIII, complete cds.// 1.70E-39// 126aa// 67%// AB026805
- HLUNG2015418// similar to cadherin and Drosophila Fat protein; similar to
- 10 CAA60685 (PID:g1107687) [Homo sapiens].// 1.00E-139// 500aa// 91%// AAD28068
- HLUNG2015548// INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE 1 (EC 1.1.1.205) (IMP DEHYDROGENASE 1) (IMPDH-I) (IMPD 1).// 3.30E-253// 521aa// 94%// P20839
- HLUNG2016862
- HSYRA2005628// ZINC FINGER PROTEIN 195.// 1.30E-237// 426aa// 78%// 014628
- 15 IMR322001879
- IMR322007078
- IMR322008651// DNA REPAIR PROTEIN RAD51 HOMOLOG 1.// 8.40E-154// 340aa// 89%// Q06609
- IMR322013396// Homo sapiens cone photoreceptor cGMP-gated channel alpha
- 20 subunit (CNGA3) mRNA, complete cds.// 0// 638aa// 98%// AF065314
- IMR322013731// TAT-BINDING HOMOLOG 7.// 1.90E-74// 187aa// 47%// P54816
- LIVER2000247// RENAL SODIUM/DICARBOXYLATE COTRANSPORTER (NA(+)/DICARBOXYLATE COTRANSPORTER).// 2.70E-57// 243aa// 48%// Q13183
- MESAN2001770// EUKARYOTIC TRANSLATION INITIATION FACTOR 4 GAMMA (EIF-4-GAMMA)
- 25 (EIF-4G) (EIF4G) (P220).// 4.70E-185// 420aa// 86%// Q04637
- MESAN2005303// DNA BINDING PROTEIN URE-B1 (EC 6.3.2.-).// 2.80E-36// 171aa// 46%// P51593
- MESAN2014412// Mus musculus zfh-4 mRNA for zinc-finger homeodomain protein 4, complete cds.// 2.8e-317// 606aa// 92%// AB024499
- 30 MESAN2015501// ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).// 7.80E-222// 753aa// 52%// Q05481
- NT2R12005772// Rattus norvegicus mRNA for DLG6 alpha, complete cds.// 4.30E-176// 273aa// 75%// AB030499
- NT2R12008952// ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).// 1.40E-
- 35 131// 393aa// 55%// P51523

- NT2R12009583// Homo sapiens orphan G-protein coupled receptor (GPC5C) mRNA, complete cds.// 3.70E-241// 441aa// 100%// AF207989
- NT2R12018448// AE-binding protein 2 [Mus musculus]// 1.00E-153// 258aa// 92%// NM\_009637
- 5 NT2R12027157// Mouse SDR2 mRNA, complete cds.// 3.20E-233// 539aa// 77%// D50464
- NT2R13000174// Homo sapiens HepA-related protein HARP mRNA, complete cds.// 1.00E-38// 136aa// 46%// NP\_054859.1
- NT2R13001132// Mus musculus Arkadia (Arkadia) mRNA, complete cds.// 0// 994aa// 90%// AF330197
- 10 NT2R13002557
- NT2R13005928
- NT2R13007167
- NT2R13007443// MITOGEN-ACTIVATED PROTEIN KINASE KINASE KINASE 5 (EC 2.7.1.-) (MAPK/ERK KINASE KINASE 5) (MEK KINASE 5) (MEKK 5) (APOPTOSIS SIGNAL-REGULATING KINASE 1) (ASK-1).// 9.50E-244// 606aa// 66%// Q99683
- 15 NT2RP7008435// EPITHIN (EC 3.4.21.-).// 6.60E-79// 354aa// 43%// P56677
- NT2RP8000521
- NTONG2008093// 6PF-2-K/FRU-2, 6-P2ASE BRAIN/PLACENTA-TYPE ISOZYME [INCLUDES: 6- PHOSPHOFRUCTO-2-KINASE (EC 2.7.1.105); FRUCTOSE-2,6-BISPHOSPHATASE (EC 3.1.3.46)].// 1.60E-72// 143aa// 97%// Q16875
- 20 OCBBF2003327// ADAM-TS 6 precursor (EC 3.4.24.-) (A disintegrin and metalloproteinase with thrombospondin motifs 6) (ADAMTS-6) (ADAM-TS6).// 2.00E-63// 108aa// 51%// Q9UKP5
- 25 OCBBF2005433// N-CHIMAERIN (NC) (N-CHIMERIN) (ALPHA CHIMERIN) (A-CHIMAERIN).// 7.70E-24// 213aa// 33%// P30337
- OCBBF2006987
- OCBBF2008144// ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).// 5.50E-244// 757aa// 56%// Q05481
- 30 OCBBF2009583// ZINC FINGER PROTEIN 184 (FRAGMENT).// 1.20E-75// 345aa// 36%// Q99676
- OCBBF2011669// Zinc finger protein 91 (Zinc finger protein HTF10) (HPF7).// 1.00E-90// 222aa// 26%// Q05481
- OCBBF2019684// ZINC FINGER PROTEIN 29 (ZFP-29).// 6.90E-246// 465aa// 90%// Q07230
- 35



- OCBBF2020048// 95 kDa retinoblastoma protein binding protein; KIAA0661 gene product // 9.90E-97// 339aa// 63%// XP\_010492
- OCBBF2024284// GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN 12.3 (P205) (RECEPTOR OF ACTIVATED PROTEIN KINASE C 1) (RACK1).// 1.60E-72//
- 5 135aa// 99%// P25388
- OCBBF2030116
- OCBBF2032274// Zinc finger protein 93 (Zinc finger protein HTF34) (Fragment).// 1.00E-145// 247aa// 67%// P35789
- OCBBF2034637// microtubule associated testis specific serine/threonine
- 10 protein kinase [Mus musculus]// 0// 450aa// 79%// NP\_032667
- OCBBF3000167// ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).// 5.00E-156// 405aa// 62%// P51522
- OCBBF3002654// Triple functional domain protein (PTPRF interacting protein).// 0// 510aa// 93%// 075962
- 15 OCBBF3003761
- OCBBF3004972
- PERIC2007068// Mus musculus mRNA for 1A13 protein.// 3.30E-121// 385aa// 62%// X83587
- PLACE7000333
- 20 PLACE7000502// Human Notch4 (hNotch4) mRNA, complete cds.// 0// 666aa// 99%// U95299
- PROST2000452// TRANSMEMBRANE PROTEASE, SERINE 2 (EC 3.4.21.-).// 1.60E-47// 186aa// 50%// 015393
- PROST2009320// enigma protein; LIM domain protein [Homo sapiens]// 6.00E-42//
- 25 77aa// 71%// NM\_005451
- PROST2019487
- PUAEN2006335
- SKMUS2003194
- SPLEN2004611// Homo sapiens transcription factor 7-like 2 (T-cell specific, HMG-box) (TCF7L2).// 1.00E-19// 50aa// 47%// NM\_030756
- 30 SPLEN2016135// Zinc finger protein 2 (Zfp-2) (mKR2 protein).// 6.00E-27// 64aa// 39%// P08043
- SPLEN2016781// zinc finger transcription factor REST protein // 5.00E-18// 80aa// 33%// AAB94893
- 35 SPLEN2016932

- SPLEN2030847// Mus musculus Kif21b (Kif21b) mRNA, complete cds.// 1.00E-85// 110aa// 94%// AF202893
- SPLEN2033490
- SPLEN2036702// TENSIN.// 8.30E-175// 409aa// 54%// Q04205
- 5 SPLEN2037319
- SPLEN2039311// Pro-Pol-dUTPasepolyprotein.\*// 2.70E-15// 93aa// 53%// 002711\*
- SPLEN2039379// Homo sapiens phosphatidylinositol 4-kinase 230 (pi4K230) mRNA, complete cds.// 0// 645aa// 99%// AF012872
- 10 STOMA2003158// DEOXYRIBONUCLEASE GAMMA PRECURSOR (EC 3.1.21.-) (DNASE GAMMA) (DEOXYRIBONUCLEASE I-LIKE 3) (DNASE I HOMOLOGOUS PROTEIN DHP2) (LIVER AND SPLEEN DNASE) (LS-DNASE) (LSD).// 5.40E-143// 267aa// 99%// Q13609
- STOMA2004893
- SYNOV1000256// Human preferentially expressed antigen of melanoma (PRAME) mRNA, complete cds.// 2.80E-29// 275aa// 35%// U65011
- 15 SYNOV2001660
- SYNOV2006620
- SYNOV2013637// Homo sapiens putative renal organic anion transporter 1 (hROAT1) mRNA, complete cds.// 2.40E-54// 213aa// 53%// AF057039
- SYNOV2021953// hematopoietic zinc finger [Mus musculus]// 1.00E-63// 300aa// 51%// NP\_038894
- 20 SYNOV4002744// Zinc finger protein 84 (Zinc finger protein HPF2).// 2.00E-26// 75aa// 30%// P51523
- SYNOV4003981// megakaryocyte stimulating factor [Homo sapiens]// 0// 400aa// 74%// NM\_005807
- 25 SYNOV4005739
- SYNOV4005889
- TBAES2000932// sirtuin 7; sirtuin type 7; silent mating type information regulation 2, S.cerevisiae, homolog 7; sir2-related protein type 7 [Homo sapiens]// 1.00E-69// 120aa// 93%// NM\_016538
- 30 TESOP2000390// Mitogen-activated protein kinase kinase kinase 14 (EC 2.7.1.37) (NF-kappa beta-inducing kinase) (Serine/threonine protein kinase NIK) (HsNIK).// 0// 354aa// 81%// Q99558
- TESOP2001796// RING finger protein 19 (Dorfin) (Double ring-finger protein) (p38 protein).// 0// 320aa// 69%// Q9NV58
- 35 TESOP2005199// ZINC FINGER PROTEIN 7 (ZINC FINGER PROTEIN KOX4) (ZINC FINGER PROTEIN HF.16).// 8.40E-104// 317aa// 49%// P17097

- TESOP2006398// zinc finger-like; similar to P52742 (PID:g1731411) [Homo sapiens].// 4.00E-22// 100aa// 97%// AAC36300
- TESOP2006865// ZINC FINGER PROTEIN MFG-3.// 5.30E-29// 116aa// 55%// P16374
- TESOP2007384// Mus musculus putative purine nucleotide binding protein mRNA,  
 5 complete cds.// 1.00E-78// 288aa// 55%// U44731
- TESTI1000266
- TESTI2008901
- TESTI2015626// Human mRNA for phosphoribosypyrophosphate synthetase-associated protein 39, complete cds.// 1.00E-181// 356aa// 99%// D61391
- 10 TESTI2025924// CASEIN KINASE I, EPSILON ISOFORM (EC 2.7.1.-) (CKI-EPSILON).// 1.80E-42// 265aa// 36%// P49674
- TESTI2026647// PROBABLE ATP-DEPENDENT RNA HELICASE DDX10 (DEAH BOX PROTEIN 10).// 6.40E-48// 226aa// 45%// Q13206
- TESTI2029252// Homo sapiens mRNA for LAK-4p, complete cds.// 2.40E-79//  
 15 410aa// 38%// AB002405
- TESTI2032643// ADENYLATE CYCLASE, TYPE IV (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (ADENYLYL CYCLASE).// 1.00E-176// 155aa// 75%// P26770
- TESTI2034251// ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).// 3.10E-186// 546aa// 57%// Q05481
- 20 TESTI2035981
- TESTI2036288// PROSTAGLANDIN-F SYNTHASE 1 (EC 1.1.1.188) (PGF SYNTHASE 1) (PGF 1) (PROSTAGLANDIN-D2 11 REDUCTASE 1) (PGFS1).// 1.10E-41// 120aa// 69%// P05980
- TESTI2037830
- 25 TESTI2039060// MALTASE-GLUCOAMYLASE, INTESTINAL [INCLUDES: MALTASE (EC 3.2.1.20) (ALPHA-GLUCOSIDASE); GLUCOAMYLASE (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE)].// 8.60E-287// 641aa// 77%// 043451
- TESTI2049956// Vegetatible incompatibility protein HET-E-1.// 5.00E-43// 107aa// 34%// Q00808
- 30 TESTI2050780// organic anion transporter OATP-E [Homo sapiens]// 4.00E-28// 71aa// 34%// NM\_016354
- TESTI4000137
- TESTI4000155
- TESTI4000183// ZINC FINGER PROTEIN 177.// 4.60E-66// 299aa// 43%// Q13360
- 35 TESTI4000214// similar to human transcription factor TFIIS (S34159)// 7.00E-40// 400aa// 32%// BAA13438

- TESTI4000319// GUANINE NUCLEOTIDE DISSOCIATION STIMULATOR RALGDS FORM B (RALGEF).// 4.70E-50// 256aa// 48%// Q03386
- TESTI4001984
- 5 TESTI4005317// Homo sapiens rab6 GTPase activating protein (GAP and centrosome-associated) (GAPCENA), mRNA// 0// 536aa// 95%// NM\_012197
- TESTI4006473// ATP-dependent RNA helicase A (Nuclear DNA helicase II) (NDH II) (DEAD-box protein 9).// 5.00E-72// 208aa// 33%// Q28141
- TESTI4008058
- 10 TESTI4008302// zinc finger protein [Homo sapiens]// 0// 382aa// 89%// NM\_014347
- TESTI4010382// cytoplasmic dynein heavy chain 2 [Rattus norvegicus]// 0// 1171aa// 90%// NM\_023024
- TESTI4011070// Glucoamylase S1/S2 precursor (EC 3.2.1.3) (Glucan 1,4-alpha-glucosidase) (1,4-alpha-D-glucan glucohydrolase).// 5.00E-18// 148aa// 20%// P08640
- 15 TESTI4011072// tudor domain containing 1 [Mus musculus]// 1.00E-38// 201aa// 22%// NM\_031387
- TESTI4011829
- TESTI4013365// S-antigen protein precursor.// 6.00E-07// 109aa// 20%// Q03400
- 20 TESTI4013602
- TESTI4013894// mitsugumin 29 [Mus musculus]// 1.00E-117// 200aa// 92%// NM\_008596
- TESTI4014801// novel protein similar to archaeal, yeast and worm N2, N2-dimethylguanosine tRNA methyltransferase [Homo sapiens]// 0// 312aa// 89%// NM\_030934
- 25 TESTI4015012
- TESTI4015442// zinc finger homeodomain 4 [Mus musculus]// 0// 875aa// 79%// NM\_030708
- TESTI4017714// Protease II (EC 3.4.21.83) (Oligopeptidase B).// 4.00E-52// 175aa// 25%// Q59536
- 30 TESTI4019657// cyclin G associated kinase [Homo sapiens]// 1.00E-138// 311aa// 88%// NP\_005246
- TESTI4021482// RAC-alpha serine/threonine kinase (EC 2.7.1.-) (RAC-PK-alpha) (Protein kinase B) (PKB) (C-AKT).// 3.00E-28// 58aa// 98%// P31749
- 35 TESTI4024387// RAB GDP dissociation inhibitor alpha (RAB GDI alpha) (GDI-1).// 1.00E-102// 179aa// 98%// P50398

- TESTI4025268// 77 kDa echinoderm microtubule-associated protein.// 1.00E-45//  
119aa// 31%// Q26613
- TESTI4025494// Zinc finger protein 33A (Zinc finger protein KOX31)  
(HA0946).// 0// 384aa// 49%// Q06730
- 5 TESTI4025547// double-stranded RNA-binding zinc finger protein JAZ [Homo  
sapiens]// 1.00E-161// 279aa// 87%// NM\_012279
- TESTI4025865
- TESTI4026207// Kinesin-like protein KLP1.// 1.00E-83// 167aa// 43%// P46870
- TESTI4028938// Zinc finger protein 85 (Zinc finger protein HPF4) (HTF1).//  
10 0// 373aa// 66%// Q03923
- TESTI4028958
- TESTI4029348
- TESTI4029528
- TESTI4029690
- 15 TESTI4031745// Mitogen-activated protein kinase kinase kinase 5 (EC 2.7.1.-)  
(MAPK/ERK kinase kinase 5) (MEK kinase 5) (MEKK 5) (Apoptosis signal-  
regulating kinase 1) (ASK-1).// 0// 447aa// 58%// Q99683
- TESTI4032090
- TESTI4032112// Homo sapiens general transcription factor IIIC, polypeptide 1  
20 (alpha subunit, 220kD) (GTF3C1), mRNA// 1.00E-121// 213aa// 82%// NM\_001520
- TESTI4036767
- TESTI4038721
- TESTI4041086
- TESTI4046240// sirtuin 7// 1.00E-115// 44aa// 98%// NP\_057622
- 25 THYMU2004139// WEE1-LIKE PROTEIN KINASE (EC 2.7.1.112).// 2.80E-137// 534aa//  
54%// P47817
- THYMU2004284// UBIQUITIN-ACTIVATING ENZYME E1 (A1S9 PROTEIN).// 9.00E-63//  
122aa// 100%// P22314
- THYMU2006001// ZINC-BINDING PROTEIN A33.// 8.40E-51// 476aa// 27%// Q02084
- 30 THYMU2028739// ZINC FINGER PROTEIN 263 (ZINC FINGER PROTEIN FPM315).// 1.10E-  
39// 291aa// 40%// 014978
- THYMU2030462
- THYMU2031139// Homo sapiens zinc metalloprotease ADAMTS7 (ADAMTS7) mRNA,  
complete cds.// 3.30E-105// 504aa// 42%// AF140675
- 35 THYMU2031249// SERINE/THREONINE-PROTEIN KINASE PCTAIRE-1 (EC 2.7.1.-).//  
1.20E-138// 291aa// 92%// Q00536

- THYMU2032976  
 THYMU2033401  
 THYMU2034279  
 THYMU2035078// LRP16 protein [Homo sapiens]// 3.00E-50// 80aa// 55%//  
 5 NP\_054786  
 THYMU2035710// Tyrosine-protein kinase-like 7 [Precursor]// 1.00E-50//  
 121aa// 80%// Q13308  
 THYMU2040925// CDP-DIACYLGLYCEROL--INOSITOL 3-PHOSPHATIDYLTRANSFERASE (EC  
 2.7.8.11) (PHOSPHATIDYLINOSITOL SYNTHASE) (PTDINS SYNTHASE) (PI SYNTHASE).//  
 10 4.60E-50// 118aa// 86%// O14735  
 THYMU3000269// SUCCINATE DEHYDROGENASE [UBIQUINONE] FLAVOPROTEIN SUBUNIT,  
 MITOCHONDRIAL PRECURSOR (EC 1.3.5.1) (FP) (FLAVOPROTEIN SUBUNIT OF COMPLEX  
 II).// 2.80E-130// 245aa// 99%// P31040  
 THYMU3000360  
 15 THYMU3001428  
 TKIDN2008778  
 TKIDN2012771// DPY-19 PROTEIN.// 5.30E-49// 314aa// 35%// P34413  
 TKIDN2018926  
 TLIVE2001684// complement component 3 precursor [Homo sapiens]// 5.00E-59//  
 20 110aa// 32%// NP\_000055  
 TLIVE2002046// DELTA-AMINOLEVULINIC ACID DEHYDRATASE (EC 4.2.1.24)  
 (PORPHOBILINOGEN SYNTHASE) (ALADH).// 3.10E-156// 317aa// 93%// P13716  
 TLIVE2007607// CYTOCHROME P450 4A4 (EC 1.14.14.1) (CYP1A4) (PROSTAGLANDIN  
 OMEGA- HYDROXYLASE) (P450-P-2).// 6.90E-127// 448aa// 49%// P10611  
 25 TRACH1000212  
 TRACH2000862// Mus musculus putative purine nucleotide binding protein mRNA,  
 complete cds.// 5.40E-224// 619aa// 68%// U44731  
 TRACH2007483// GASTRULA ZINC FINGER PROTEIN XLCGF7.1 (FRAGMENT).// 6.30E-12//  
 98aa// 37%// P18735  
 30 TRACH2019672// Rattus norvegicus mRNA for 45 kDa secretory protein,  
 partial.// 5.80E-163// 303aa// 96%// AJ132352  
 TRACH2024408// ankyrin 2, isoform 2; ankyrin-2, nonerythrocytic; ankyrin-B;  
 ankyrin, brain; ankyrin, neuronal; ankyrin, nonerythroid [Homo sapiens]//  
 1.00E-06// 119aa// 20%// NM\_020977  
 35 TRACH2024559// Homo sapiens myosin 5c (MYO5C) mRNA, complete cds.// 1.70E-  
 59// 151aa// 86%// AF272390

- TRACH3000134// ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).// 2.30E-215// 733aa// 53%// P51523
- TRACH3000420// Homo sapiens ATP-binding cassette transporter family A member 12 (ABCA12) mRNA, complete cds.// 7.00E-253// 745aa// 41%// AY033486
- 5 TRACH3002561// UNR protein.// 2.00E-34// 66aa// 95%// P18395
- TRACH3003683// Lactoperoxidase precursor (EC 1.11.1.7) (LPO) (Salivary peroxidase) (SPO).// 1.00E-39// 77aa// 86%// P22079
- TRACH3003832// PHD finger protein 2 [Mus musculus]// 1.00E-153// 321aa// 39%// NM\_011078
- 10 TRACH3007866// dipeptidyl peptidase 8; hypothetical protein FLJ20283 [Homo sapiens]// 1.00E-105// 172aa// 53%// NM\_017743
- TUTER2000057// Mus musculus AE-1 binding protein AEBP2 mRNA, complete cds.// 1.10E-26// 60aa// 93%// AF090326 ---
- UTERU2004299
- 15 UTERU2008040// Mus musculus mRNA for stac, complete cds.// 3.30E-82// 405aa// 47%// D86639
- UTERU2011220
- UTERU2019534// Golgi apparatus protein 1 [Homo sapiens]// 5.10E-61// 118aa// 100%// XP\_012515
- 20 UTERU2021820// dipeptidylpeptidase VI [Homo sapiens]// 8.00E-23// 50aa// 89%// NP\_001927
- UTERU2028734// Mus musculus slp2-a mRNA for synaptotagmin-like protein 2-a delta 2S-III, complete cds.// 2.30E-216// 464aa// 86%// AB057762
- UTERU2032279// 47 KDA HEAT SHOCK PROTEIN PRECURSOR (COLLAGEN-BINDING PROTEIN
- 25 1) (COLLIGIN 1).// 6.90E-95// 207aa// 93%// P29043
- UTERU2033577// Homo sapiens mRNA for repressor protein, partial cds.// 1.80E-65// 209aa// 65%// D30612
- UTERU2035978
- UTERU3000402
- 30 UTERU3000738// Beta-adrenergic receptor kinase 1 (EC 2.7.1.126) (Beta-ARK-1) (G- protein coupled receptor kinase 2).// 5.00E-76// 139aa// 94%// P26817
- UTERU3001053// zinc finger protein [Homo sapiens]// 0// 319aa// 91%// NM\_018651
- UTERU3014791
- 35 UTERU3015069
- UTERU3015412

UTERU3017176

TEST14038779// zinc finger protein RIN ZF [Rattus norvegicus]// 3.00E-73//

190aa// 36%// NM\_024489